

801
BEST AVAILABLE COPY

74996

9/6 02

Access DB#

CRF

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Nimal S. Bosi Examiner #: _____ Date: 9/5/02
Art Unit: _____ Phone Number 30 89435 Serial Number: 09/827937
Mail Box and Bldg/Room Location: CM1 10E17 Results Format Preferred (circle): PAPER-DISK E-MAIL
Mail on 10019

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Human G-Protein coupled Receptor
Inventors (please provide full names): Li et al

Earliest Priority Filing Date: 5/7/97

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Mean search
1 SEQ ID NO: 2

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 6A04
703-308-3534

Unmerged + issued + interference data base

RECEIVED
SEP -5 2002
CHEM. S.
(STIC)

Prot 2

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: _____	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>9/3</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>9/9</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>12</u>	Fulltext _____	Sequence Systems <u>AS</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: <u>12</u>	Other _____	Other (specify) _____

as Page Blank (uspto)

PA (HUMA-) HUMAN GENOME SCI INC.

PI Li Y, Ruben SM;

DR WPI; 1999-034722/03.

DR N-PSDB; AAV69760.

PT New Isolated human G-protein coupled receptors - used to develop
PT products for treating e.g. asthma, Parkinson's disease, heart
PT failure, osteoporosis, hypertension, psychoses, eating disorders or
PT cancers

PS Claim 1; Fig 1A-C; 65pp; English.

CC This represents a EBV-induced G-protein coupled receptor (EBI-2)
CC polypeptide. The encoding DNA is deposited under the accession number
CC ATCC No: 209003. The invention provides two human G-protein coupled
CC receptor polypeptides. The polypeptides are human Epstein-Barr Virus
CC (EBV)-induced G-protein coupled receptor, designated EBI-2 polypeptide
CC and a human endothelium-differentiation gene (EDG) like G-protein coupled
CC receptor, designated EDS-1-like G-protein coupled receptor. Vectors
CC comprising the EBI-2 and EDS-1-like polypeptides encoding DNA can be used
CC to transform host cells for the recombinant production of the proteins.
CC Agonists for G-protein coupled receptors can be used for the treatment of
CC asthma, Parkinson's disease, acute heart failure, hypotension, urinary
CC retention and osteoporosis. Antagonists can be used for the treatment of
CC hypertension, angina pectoris, myocardial infarction, ulcers, asthma,
CC allergies, psychoses, depression, migraine, vomiting, stroke, eating
CC disorders, migraine headaches, cancer and benign prostatic hypertrophy.
CC The products can also be used for detection, diagnosis and drug
CC screening.

Sequence 342 AA;

Query Match	100.0%;	Score 1778;	DB 20;	Length 342;
Best Local Similarity	100.0%;	Pred. No. 4.2e-187;		
Matches 342;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MONDNLTLSAGSNSTLGRDVKIKQVLFPLLTYVTLFVGLITNGLARIFQIRSKNFI	60
Db	1	mqadvnltsapgnslcrdykllcqvlfpillyvllfvtglltnglamrlffqirsknfl	60
QY	61	IFLNKVTISDMLITLPEFKLTSDAKIGTGPLRPFVCOVSVIEPFMYTISISPLGITIT	120
Db	61	iflnkvtisdlmlitlfpikllsdaklgcplrltrvcqvsvilyitmytisistlglitl	120
QY	121	DRYQRTPEFTSNPKNLGAKISVYIWAAMFLSLPNMILTNRQDRDKNVKCSFLKS	180
Db	121	dryqtrtpeftsnpknlgakllsvyiwatmfllslpmlltlnrprdknvkcsflks	180
QY	181	EFGWLMEIVNYICQVIFWINEFLIVICYTLITKELYRSYVRPGVGRKRVKVVFI	240
Db	181	efglwmeivnylqcvlfwlnflivrcylitkelyrsyvrtrgygkvrpkknkvfl	240
QY	241	IIA VFICVFPFHARIPYTLISQTRVDCTAENTLFYVKESTLWLTSLNACDPEITYFF	3000
Db	241	iiavflicfvpfharrpytlisqrtdctcaentlfiykestlwltslnacdpeifyff	3000
QY	301	LCKSFRNLSLMLCKPNSATISLSDNKRKEDGGDGNPEETPM	342
Db	301	lcksfmrnlsmlckpnsatlsldnkrkedggdgnpeetpm	342

RESULT 2

ID AAY71306 standard; Protein; 342 AA.

AC AAY71306;

DT: 02-NOV-2000 (first entry)

DE Human orphan G protein-coupled receptor hCHN8

XX Human; orphan G protein-coupled receptor; GPCR; hGHN8; drug screening,
KW transmembrane receptor; expressed sequence tag; EST; signal cascade.
KW

OS Homo sapiens.

PN W0200031258-A2.

PD 02-JUN-2000.

PF 13-OCT-1999; 99WO-US23687

PR	20-OCT-1998	9805-01029.13
PR	16-FEB-1999	9905-01040.16
PR	26-FEB-1999	9905-012185.2
PR	12-MAR-1999	9905-012384.6
PR	12-MAR-1999	9905-012384.9
PR	28-MAY-1999	9905-013643.36
PR	28-MAY-1999	9905-013643.37
PR	28-MAY-1999	9905-013646.39
PR	28-MAY-1999	9905-013653.67
PR	28-MAY-1999	9905-013713.91
PR	28-MAY-1999	9905-013712.27
PR	28-MAY-1999	9905-013713.31
PR	28-JUN-1999	9905-014144.8
PR	28-SEP-1999	9905-015655.55
PR	28-SEP-1999	9905-015663.33
PR	29-SEP-1999	9905-015663.34
PR	29-SEP-1999	9905-015665.53
PR	01-OCT-1999	9905-015728.80
PR	01-OCT-1999	9905-015728.81
PR	01-OCT-1999	9905-015728.82
PR	01-OCT-1999	9905-015729.84
PR	01-OCT-1999	9905-015729.84
PR	12-OCT-1999	9905-041670.4
PR	12-OCT-1999	9905-041704.4

PA (AREN-) ARENA PHARM INC

PI Chen R, Dang HT, Liaw CW, Lin I;

DR WPI; 2000-400068/34

DR N-PSDB; AAD01133.

PT Novel human orphan G protein-coupled receptors and the encoding cDNAs
PT for use in the identification of G protein-coupled receptor agonists -
XX
PS Claim 62; Page 82-83; 102pp; English.

CC The present amino acid sequence of the hGPR8, an endogenous human
CC orphan G protein-coupled receptor (GPCR), expressed in left and right
CC cerebellum, kidney and lung. The hGPR8 cDNA was identified using full
CC length EST (expressed sequence tag) 764455 as a probe.
CC The orphan GPCR of the invention, like all GPCRs has seven transmembrane
CC alpha helices with an extracellular N-terminus and an intracellular
CC C-terminus. However, no endogenous ligands has yet been identified for
CC the proteins of the invention. The orphan GPCRs may be used in the
CC identification of their endogenous ligands, and to screen potential GPCR
CC agonists and antagonists for use as pharmaceutical agents. The proteins
CC may also be used in the study of GPCR-mediated signalling cascades, and
CC to elucidate their precise role in normal and diseased human conditions.
CC Nucleic acid encoding human orphan GPCRs may be used for tissue
CC localisation expression analysis to provide information about their
CC function in healthy and pathological states.

50 Sequence 342 AA;

Query Match	100.0%	Score 1778;	DB 21;	Length 342;
Best Local Similarity	100.0%	Pred. No. 4.2e-187;		
Matches 342;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

```
0Y      1 MQAVDNLTSAPGNTSLCTRDYKTKTVLFFPLTYLVFFVGLITNGLAMRIFFQIISKSNFI 600
|||||
```


Query	Best Match	Similarity	Score	DB	Length	342:
1	MOAVDNILTSAGGNTSLCYRDYKKTQVLEPLLYTVLFFVGLITNGLANRIFPOIRKSNFI	60				
2	1 mgavonltsapngslscrdykitqivlfpillyrvlffgltlnglanriffigtsksnfi	60				
3	1 IFKNTVTSIDLLMITFPFKILSDAKLTGGLRFPVCOVSVIFFTMYTISISFLGLITI	120				

Db	61	iflknltvlsdlmlitlftfkrlksdaklsgpbrlrtfcvqgsvsfiyfmytsisflgltl	120
Oy	121	DEYQKTRPREKNSNPENLUGAKTLSTVIAFMFLLSPNNLILNROPBKNVVKCSPLKS	180
Db	121	dryqkcltupfkfksupnlllgakllsvlvaafmlslsppmlilnrgprdknkvksclks	180
Oy	181	ENGLVWHEILVANYICQYIEMINFLIVCYTLITLKELYSRVYTRGVGRVPRKKVNVKEFI	240
Db	181	egflwvheivnylqglifwlnflivaycytlitkelyrsyvrtrcygkvpkrkknvkvfi	240
Oy	241	ITAVPFICVPRPHFARIPFTLSQTRVPOCTANRTLFYKVESTLMLTSLWACDPFIYFF	300
Db	241	llavfficvprphfariptylsqtrvfdctaenrlfyvestclwtslnacdpliyff	300
Oy	301	LKSFERNLSIMLKCPNSATSLSDQNRKKEODCGDNEETPM	342
Db	301	lksfrrnlsimlkcpnsatslsqdnrkkegdgdpneetpm	342
RESULT 5			
ID	AAM79249		
xx	AAM79249 standard; Protein; 342 AA.		
AC	AAM79249;		
DT	06-NOV-2001 (first entry)		
xx			
DE	Human protein SEQ ID NO 1911.		
xx			
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;		
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;		
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;		
xx	lissous system disorder; arthritis; inflammation.		
OS	Homo sapiens.		
xx			
PN	WO200157190-A2.		
PD	09-AUG-2001.		
xx			
PF	05-FEB-2001; 2001WO-US04098.		
xx			
PR	03-FEB-2000; 2000US-0496914.		
PR	27-APR-2000; 2000US-0560875.		
PR	20-JUN-2000; 2000US-0598075.		
PR	19-JUL-2000; 2000US-0620325.		
PR	01-SEP-2000; 2000US-0654936.		
PR	15-SEP-2000; 2000US-0663561.		
PR	20-OCT-2000; 2000US-0693325.		
PR	30-NOV-2000; 2000US-0728422.		
xx			
PA	(HISE-) HISEQ INC.		
xx			
PI	Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;		
PI	Zhao Qa, Wang D, Wang Y, Zhang J, Ren F, Chen R, Wang ZW;		
PI	Xue AJ, Yang Y, Wejhrman T, Goodrich R;		
xx			
DR	WPI: 2001-476283/51.		
xx	N-PSDB; AAK52382.		
PT			
PT	Nucleic acids encoding polypeptides with cytokine-like activities,		
xx	useful in diagnosis and gene therapy -		
xx			
PS	Claim 20; Page 4310; 6221pp; English.		
xx			
CC	The invention relates to polynucleotides (AAK51456-AAK53435) and the		
CC	encoded polypeptides (AAM78323-AAW80302) that exhibit activity elating to		
CC	cytokine, cell proliferation or cell differentiation or which may induce		
CC	production of other cytokines in other cell populations. The		
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or		
CC	peptide therapy. The polypeptides have various cytokine-like activities,		
CC	e.g. stem cell growth factor activity, haematopoiesis regulating		
CC	activity, tissue growth factor activity, immunomodulatory activity and		

activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis, and inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666, (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.

Query Match 100.0%; Score 1778; DB 22; Length 342;
 Best Local Similarity 100.0%; Pred. No. 4.2e-187; Indels 0; Gaps 0;
 Matches 342; Conservative 0; Mismatches 0;

1 MQAVDNLTSAPGNTSLCTRDYKITYQLVPLTYVFFVGLITNGLAMRIFFOIRKSNFI 60
 1 mqavdnltspgntslctrdykitqvlpltyvffvglitnglamrffqirsksnfi 60
 61 IFKNTVISDLMLTFPPFKILSDAKLGTPURTEVCQVTSVIFFTWYISIFGLITTI 120
 61 ifkntvisdlmltffpkilsdaklgtpurtevcqvtswifftwyisifglit 120
 121 DRYOKTRPFKTSNPKNLGAKILSVYIMAFNMLSLPNMILTRNOPRKNVKKSEFLKS 180
 121 dryoktrpfktsnpknlgakilsvyimafnmlslpnmiltnrpnkvnkksflks 180
 181 EFGLVWHEIYNYICOVIFNFIIVCYTLITKELRSYVTRGVGKVPKRVKVKFI 240
 181 efglvwheinyicovifnfnliivcytlitkelyrsyvrtrgvgkvpkrvkvkfi 240
 241 IIAVFICVFPFHARIPYTLISQTRVDCTAENTLFYVKESTLWLTSLNACDPFIYFF 300
 241 iiavficvfpfharipytlisqtrvdcntaentlfyvestlwltslnacdpfiyff 300
 301 LCKSPRNLISMLKCPNSATSLSDNNRKEQDGPNEHPPM 342
 301 lcksprnlismlkcpnsatsslodnnrkeqdgdpneehppm 342

RESULT 6
 AAE04386
 ID AAE04386 standard; Protein: 342 AA.
 AC AAE04386;
 DT 04-SEP-2001 (first entry)

Human P2-purine receptor subtype, P2Y12.

Human: P2-purine receptor; P2Y12; cardiant; vasotropic; thrombolytic; cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina; myocardial infarction; ischaemic attack; preclampsia; brain disorder; migraine; carotid endarterectomy; vascular graft surgery; depression; angiolysis; vascular injury; schizophrenia; eating disorder; depression; embolism; peripheral vascular disease; platelet aggregation; resenotic; embolism; thrombocytopenic purpura; stroke; pertussis toxin sensitive G protein; GI; disseminated intravascular coagulation; thrombosis.

OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Domain 27..50
 FT Domain 58..82
 FT Domain 97..121
 FT Domain 140..163
 FT Domain 189..213
 FT Domain 234..259
 FT Domain 278..303

Domain 278..303
 /label= Transmembrane-domain_7
 WO200146454-A1.
 28-JUN-2001.
 26-DEC-2000; 2000WO-US34998.
 23-DEC-1999; 99US-0171622.
 (COR-) COR THERAPEUTICS INC.
 Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;
 Holloper G;
 WPI: 2001-418052/44.
 N-PSDB: AAD08695.

Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful for identifying binding partners and for diagnostic applications -
 Example 1, Fig 5A; 108pp; English.

The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is the subtype of P2-purine receptor and brain, and couples to a pertussis toxin-sensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor that responds to ADP. The invention also relates to a method for identifying an agent which is useful for modulating acute myocardial infarction, unstable angina, chronic stable angina, transient ischaemic attacks, strokes, peripheral vascular disease, preclampsia, deep venous thrombosis, embolism, disseminated intravascular coagulation, thrombotic cerebrocytopenic purpura or a bleeding disorder; carotid endarterectomy, stent CABG (coronary artery bypass graft) surgery, vascular graft surgery, post CABG (coronary artery bypass graft) surgery, and for screening P2Y12 receptor is useful for identifying binding partners and for diagnostic applications. P2Y12 receptor provides targets for screening diagnostic small molecules and combinatorial or naturally occurring compound libraries to regulate platelet aggregation, depression, migraine disease as well as schizophrenia, eating disorders, depression, migraine and other brain disorders. The present sequence is human P2-purine receptor subtype, referred as P2Y12.

Sequence 342 AA;

Query Match 100.0%; Score 1778; DB 22; Length 342;
 Best Local Similarity 100.0%; Pred. No. 4.2e-187; Indels 0; Gaps 0;
 Matches 342; Conservative 0; Mismatches 0;

1 MQAVDNLTSAPGNTSLCTRDYKITYQLVPLTYVFFVGLITNGLAMRIFFOIRKSNFI 60
 1 mqavdnltspgntslctrdykitqvlpltyvffvglitnglamrffqirsksnfi 60
 61 IFKNTVISDLMLTFPPFKILSDAKLGTPURTEVCQVTSVIFFTWYISIFGLITTI 120
 61 ifkntvisdlmltffpkilsdaklgtpurtevcqvtswifftwyisifglit 120
 121 DRYOKTRPFKTSNPKNLGAKILSVYIMAFNMLSLPNMILTRNOPRKNVKKSEFLKS 180
 121 dryoktrpfktsnpknlgakilsvyimafnmlslpnmiltnrpnkvnkksflks 180
 181 EFGLVWHEIYNYICOVIFNFIIVCYTLITKELRSYVTRGVGKVPKRVKVKFI 240
 181 efglvwheinyicovifnfnliivcytlitkelyrsyvrtrgvgkvpkrvkvkfi 240
 241 IIAVFICVFPFHARIPYTLISQTRVDCTAENTLFYVKESTLWLTSLNACDPFIYFF 300
 241 iiavficvfpfharipytlisqtrvdcntaentlfyvestlwltslnacdpfiyff 300

QY 301 LCKSFRNSLSMLKCPNSATSLSDNRKKEDGDPNEETPM 342
 DB 301 lcksfnsrlslsmkcpnsatslsqdnrrkkgdgdgdpneetpm 342

RESULT 7
 AAY94445
 ID AAY94445 standard; Protein; 342 AA.
 AC AAY94445;
 XX
 XX 21-AUG-2000 (first entry)

DE Macaque ortholog of human 15625 receptor protein.
 XX
 XX Human; G-protein-coupled receptor; GPCR; 15625 receptor protein;
 KW glial cells; spleen; colon; liver; brain; T-cell; heart;
 KW red cell; thymus; B-cell; pancreas; disorder; chromosome 3;
 KW anemia; neutropenia; thrombocytopenia; gene therapy; ss.
 XX
 OS Macaca sp.
 XX
 FN WO200028028-A1.
 XX
 PD 18-MAY-2000.
 XX
 PF 05-NOV-1999; 99WO-US25956.
 XX
 PR 06-NOV-1998; 98US-0187134.
 PR 25-AUG-1999; 99US-0382918.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Glucksmann MA, Gu W, Welch NS;
 DR WPI: 2000-376543/32.
 DR N-PSDB; AAA27127.
 XX

PT Identifying an agent modulating the level or activity of G-protein
 PT coupled receptor useful for screening a cell derived from a subject
 XX having disorders such as anaemia, neutropenia and thrombocytopenia
 PS Disclosure: Page 90-92; 97pp; English.
 XX

XX The 15625 receptor protein is a novel G-coupled protein receptor (GPCR).
 CC The cDNA for this protein was isolated by screening a human cDNA library
 CC with sequences homologous to other GPCRs. The 15625 receptor protein is
 CC expressed in the glial cells of the brain. It is also expressed in
 CC several other tissues. The 15625 receptor protein may be useful for
 CC producing antibodies which can be used to detect the presence of the
 CC receptor protein. The 15625 receptor protein polynucleotides are useful
 CC for generating probes, primers and antisense constructs. The
 CC polynucleotides encoding the 15625 receptor protein can also be inserted
 CC into vectors to be used in gene therapy. The disorder that may be
 CC treated using the 15625 receptor protein polynucleotides and
 CC polypeptides include anaemia, neutropenia and thrombocytopenia. The
 CC present sequence is the macaque ortholog of the human 15625 receptor
 CC protein.
 CC
 XX Sequence 342 AA;

Query Match 98.3%; Score 1748; DB 21; Length 342;
 Best Local Similarity 98.0%; Pred. No. 8 3e-184;
 Matches 333; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MQAVNLTSAAGNLSCTRYKTTQVLFPLVTLVFEVGLTNGLAMRFOIRSKSMFI 60
 DB 1 mgaidltsaprtstictdykltqvlfpilytvlffvgiltstamiffqilsksnfi 60
 QY 61 IFLKNVISDLMLILTFPRKILSDAKLGTGPRFPCOVTSVIFVYFWYISISFLGLIT 120
 DB 61 iflknvisdlmliltfprkilsdaklgtgprfpcovtsvifvfyfwyisiflglit 120

QY 121 DRYOKTTREPKTSNPNKLLGAKILSVITWAFMFLSLPMLNLRQPRDNVKKCSFLS 180
 DB 121 dryokttrpfrktsnpknllgakiilsvitwafmflslpmlnrrprdnvkcsfls 180
 QY 181 EFGLVWHEIVANICOVTFWTFWFLVIVCYTLTKELRSYVTRGVGKPRKVNKVF 240
 DB 181 efglvwheivanyicovtfwtfwflvivcytltkelrsvytrgvkgprkvnkvfi 240
 QY 241 IIAVFFICFVPHFARIPYTLSDTRDVEDCTARNTLFPYKESTLWLTSLMACLDPEIYFF 300
 DB 241 iiafficfvpfhfaripyltsdtrdvfdcaentlfykestlwltslnacldpfiyff 300
 QY 301 LCKSFRNSLSMLKCPNSATSLSDNRKKEDGDPNEETPM 342
 DB 301 lcksfnsrlslsmkcpnsatslsqdnrrkkgdgdgdpneetpm 342

RESULT 8
 AAE04385
 ID AAE04385 standard; Protein; 315 AA.
 AC AAE04385;
 XX
 XX 04-SEP-2001 (first entry)
 DE
 XX Human P2-purinegic receptor subtype, P2Y12 protein fragment.
 XX
 KW Human; P2-purinegic receptor; P2Y12; cardiac; vasotropic; thrombolytic;
 KW cerebroprotective; gynaecological; Adp; adenosine 5'-diphosphate; angina;
 KW myocardial infarction; ischemic attack; preclampsia; bleeding disorder;
 KW carotid endarterectomy; vascular graft surgery; brain disorder; migraine;
 KW vascular injury; schizophrenia; eating disorder; depression; angioplasty;
 KW peripheral vascular disease; platelet aggregation; restenosis; embolism;
 KW thrombocytopenic purpura; stroke; pertussis toxin-sensitive G protein;
 KW G; disseminated intravascular coagulation; thrombosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200146454-A1.
 XX
 PD 28-JUN-2001.
 XX
 PF 26-DEC-2000; 2000WO-US34998.
 XX
 PR 23-DEC-1999; 99US-0171622.
 XX
 PA (CORT-) COR THERAPEUTICS INC.
 XX
 PI Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;
 DR Holloper G;
 DR WPI: 2001-418082/44.
 DR N-PSDB; AAD08694.
 XX

PT Novel isolated Adp receptor, termed P2Y12 receptor polypeptide, useful
 PT for identifying binding partners and for diagnostic applications
 XX
 PS Example 1: Page 84-85; 108pp; English.
 XX

CC The invention relates to Adp (adenosine 5'-diphosphate) receptor, termed
 CC as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is
 CC the subtype of P2-purinegic receptor. The P2Y12 receptor is expressed
 CC selectively in the platelets and brain, and couples to a pertussis toxin-
 CC sensitive G protein (G_i). P2Y12 receptor is a G protein-coupled receptor
 CC that responds to Adp. The invention also relates to a method for
 CC identifying an agent which is useful for modulating acute myocardial
 CC infarction, unstable angina, chronic stable angina, transient ischemic
 CC attacks, strokes, peripheral vascular disease, preclampsia, deep venous
 CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic
 CC thrombocytopenic purpura or a bleeding disorder; restenosis; embolism;
 CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery,

CC stent placements or insertion of endovascular devices and prostheses.
CC P2Y12 receptor is useful for identifying binding partners and for
CC diagnostic applications. P2Y12 receptor provides targets for screening
CC synthetic small molecules and combinatorial or naturally occurring
CC compound libraries to regulate platelet aggregation, vascular injury, or
CC disease as well as schizophrenia, eating disorders, depression, migraine
CC and other brain disorders. The present sequence is a fragment of human
CC P2-purinergic receptor subtype, referred as P2Y12.

SQ Sequence 315 AA:

Query Match 91.9%; Score 1634; DB 22; Length 315;
Best Local Similarity 100.0%; Pred. No. 2.6e-171;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOAVDNLTSAAGNLSLCRDYKKTQVLEPLLTVLFFVGLTNGLAMRIFQIRSKSNFI 60
DB 1 mqvadnltsapgnslctrdykktqvleplltylffvgtlntglamrlffqirsksnfi 60
QY 61 IFLKNTVISDLMLITFPFKILSDAKLCTGPRFVCOVSVTFEFTWYISIFGLITFI 120
DB 61 iflknrtvisdlmlitfpfkilstdaklctgprfvcovsvtfefwtwysifglitfi 120
QY 121 DRYQKTRPEKTSNPKNLGAKILSVIWAFFLLSLPMILTNROPDKNKKCSFKS 180
DB 121 dryqktrpektspnknlgakilsvisvawaffllslpmiltntropdknkkcsfiks 180
QY 121 dtygktrtpfktsnpknlgakilsvisvawaffllslpmiltntropdknkkcsfiks 180
QY 161 EBLGWHIEIVNYICQVIFWINEFLIVCYTLITKELYSRYVTRGVGKVRKKNVYFI 240
DB 161 eblgwhieivnyicqvifwineflivcytlitkelysryvtrgvkgvrkknvfyfi 240
QY 241 IIAVEFICFVPHFARIPYTSQTRDVPECTAENTLFYKKESTLMTSLNACLDPEITVF 300
DB 241 iiaveficfvpfhfariptytsqtrdvpectaentlfykkestlmtslnacldpeitvf 300
QY 301 LCKSPFNSLSMLKC 315
DB 301 lcksfnsllsmk 315

RESULT 9

AAE04384 AAE04384 standard; Protein: 343 AA.

AC AAE04384;

DT 04-SEP-2001 (first entry)

DE Rat P2-purinergic receptor subtype, P2Y12.

KM Rat; P2-purinergic receptor; P2Y12; cardiant; vasotropic; thrombolytic;
KM cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina;
KM myocardial infarction; ischaemic attack; preclampsia; bleeding disorder;
KM carotid endarterectomy; vascular graft surgery; brain disorder; migraine;
KM vascular injury; schizophrenia; eating disorder; depression; angioplasty;
KM peripheral vascular disease; platelet aggregation; restenosis; embolism;
KM thrombocytopenic purpura; stroke; pertussis toxin-sensitive G protein;
KM G1; disseminated intravascular coagulation; thrombosis.

XX Rattus norvegicus.

XX WO200146454-A1.

XX 28-JUN-2001.

XX 26-DEC-2000; 2000WO-US34998.

XX 23-DEC-1999; 99US-0171622.

XX (COR-) COR THERAPEUTICS INC.

XX Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;

PI Holloper G;

XX WPI; 2001-418082/44.
DR N-PSDB; AAD08693.

PT Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful
PT for identifying binding partners and for diagnostic applications
PS Claim 14; Page 81-82; 108pp; English.

XX The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed
XX as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is
XX the subtype of P2-purinergic receptor. The P2Y12 receptor is expressed
XX selectively in the platelets and brain, and couples to a pertussis toxin-
XX sensitive G protein (G_i). P2Y12 receptor is a G protein-coupled receptor
XX that responds to ADP. The invention also relates to a method for
XX identifying an agent which is useful for modulating acute myocardial
XX infarction, unstable angina, chronic stable angina, transient ischaemic
XX attacks, strokes, peripheral vascular disease, preclampsia, deep venous
XX thrombosis, embolism, disseminated intravascular coagulation, thrombotic
XX thrombocytopenic purpura or a bleeding disorder; thrombotic and
XX restenotic complications following angioplasty, carotid endarterectomy,
XX post CABG (coronary artery bypass graft) surgery, vascular graft surgery,
XX stent placements or insertion of endovascular devices and for
XX P2Y12 receptor is useful for identifying binding partners and for
XX diagnostic applications. P2Y12 receptor provides targets for screening
XX synthetic small molecules and combinatorial or naturally occurring
XX compound libraries to regulate platelet aggregation, vascular injury, or
XX disease as well as schizophrenia, eating disorders, depression, migraine
XX and other brain disorders. The present sequence is rat P2-purinergic
XX receptor subtype, referred as P2Y12 receptor.

SQ Sequence 343 AA:

Query Match 86.0%; Score 1528.5; DB 22; Length 343;
Best Local Similarity 86.9%; Pred. No. 1.2e-159;
Matches 293; Conservative 17; Mismatches 22; Indels 5; Gaps 1;

QY 6 NLTSAPGNTSLCTRDYKKTQVLEPLLTVLFFVGLTNGLAMRIFQIRSKSNFI 65
DB 12 nltspgntslctrdykktqvleplltylffvgtlntglamrlffqirsksnfi 65
QY 66 TVISDLMLITFPFKILSDAKLCTGPRFVCOVSVTFEFTWYISIFGLITDRYOK 125
DB 72 tvisdmlitfpfkilstdaklctgprfvcovsvtfefwtwysifglitdryok 131
QY 126 TTRPEKTSNPKNLGAKILSVIWAFFLLSLPMILTNROPDKNKKCSFKSEFGLV 185
DB 132 ttrpекtsnpknlgakilsvisvawaffllslpmiltntropdknkkcsfiksfglv 191
QY 186 WHEIVNYICQVIFWINEFLIVCYTLITKELYSRYVTRGVGKVRKKNVYFI 245
DB 192 wheivnyicqvifwineflivcytlitkelysryvtrgvkgvrkknvfyfi 251
QY 246 FICFVPHFARIPYTSQTRDVPECTAENTLFYKKESTLMTSLNACLDPEITVF 305
DB 252 ficfvpfhfariptytsqtrdvpectaentlfykkestlmtslnacldpeitvf 311
QY 306 RNSLSMLKCPNSATSLSDNRKKEDGDPNERTPM 342
DB 312 rnsllsmkrc-----stsgankkkgqgdgdpnertpm 343

RESULT 10

AAV94498 AAV94498 standard; protein: 387 AA.

AC AAV94498;

XX 15-SEP-2000 (first entry)

XX Rat MP-10 receptor protein.

XX G-protein coupled receptor; GPCR; MP-10 receptor; rat; CNS;
KW central nervous system; spleen; anaesthetic; analgesic.
XX Rattus sp.
XX WO200034333-A1.
XX 15-JUN-2000.
XX 08-DEC-1999; 99WO-SE02302.
XX 10-DEC-1998; 98SE-0004274.
XX (ASTR) ASTRA PHARMA INC.
XX (ASTR) ASTRA AB.
XX Ahmad S, Hoffert C, Lembo P, O'Donnell D, Walker P;
XX WPI: 2000-431276/37.
XX DR N-PSDB; AAAA8642.
XX Novel G protein-coupled receptor, MP-10 receptor, useful for
XX identification of new anaesthetic and analgesic agents -
XX
XX Claim 1: Fig 2: 28pp; English.
XX
XX The present sequence is rat MP-10 receptor protein. The DNA encoding
XX this protein was identified from a rat brain stem/spinal cord cDNA
XX library. In situ hybridisation analysis showed that MP-10 receptor
XX mRNA is expressed diffusely but ubiquitously in the adult rat central
XX nervous system (CNS). The mRNA was also found in adult rat spleen.
XX MP-10 receptor protein contains several structural features
XX characteristic of a G protein coupled receptor (GPCR). MP-10
XX receptor protein is useful for identifying new anaesthetic and analgesic
XX agents. Such agents may be identified using assays designed to
XX detect agonists or antagonists capable of binding to the receptor,
XX therefore modulating intracellular signalling.
XX
XX Sequence 387 AA:
SO

Query Match 84.0%; Score 1493.5; DB 21; Length 387;
Best Local Similarity 86.4%; Pred. No. 1e-155;
Matches 287; Conservative 17; Mismatches 22; Indels 5; Gaps 1;
QY 6 NLTSAPGNLSCTRYKTIQVFPPLLYTVLFVGLITNGLAMRIFPQIRSKSNFTIFLKN 65
DB 12 ntsipgusclscrdykltqvllpytlvlfagllteqlamrffqtrsksnffllkn 71
QY 66 TVISDLMLTFPPFKILSDAKLGTPPLRTFVCQVSVIFEFMYTISIFLIGITIDRYOK 125
DB 72 tvlsdmlmltfpfkllsdaklgahltlvqgvsvcfifmytisiflglitidrylk 131
QY 126 TTRPKTSPNPKNLGAKLISLVVIAFMFLSLPNMILTRNRPDKNVKCSFLKSEFLV 185
DB 132 ttrpktspsnplgakllsvaiwafmlslpnmiltnrpkdkdtkcsflkseflv 191
QY 186 WHEIYNYCOVIFMNFILIVTCVTLIRKELYSRVRRGKGVPRKRVNKKVFIIVAF 245
DB 192 wheinyncqvifmnlivtcvtlirkelysrvrrgkvprkrvnnkvfiivaf 251
QY 246 FICFVPEHFARIPYTLISOTRDVFDCTAENTLFYKESFTLMTSLNACIDPIYFELCKSF 305
DB 252 ficfvpehfariptytlisqtravfcaenelfykessflwtslnacldpiyflcksf 311
QY 306 RNSLISMUKCNSATSLSQDNRRKEQDGGDPN 337
DB 312 rnsismukcnsatslsqdnrrkkggdpns 338

RESULT 11
AAE04387

ID AAE04387 standard; Protein; 267 AA.
XX AAE04387;
AC
XX
XX 04-SEP-2001 (first entry)
DE
XX
XX Human P2-purine receptor subtype, P2Y12 truncated allelic variant.
XX
XX Human; P2-purine receptor; P2Y12; cardiant; vasotropic; thrombolytic;
KW cerebroprotective; gynaecological; ADP; adenosine 5'-diphosphate; angina;
KW myocardial infarction; ischemic attack; preclampsia; bleeding disorder;
KW carotid endarterectomy; vascular graft surgery; brain disorder; migraine;
KW vascular injury; schizoprenia; eating disorder; depression; angioplasty;
KW peripheral vascular disease; platelet aggregation; restenotic; embolism;
KW thrombocytopenic purpura; stroke; pertussis toxin-sensitive G protein;
KW GI; disseminated intravascular coagulation; thrombosis; mutant; mutein;
KW variant.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX WO200146454-A1.
XX 28-JUN-2001.
XX 26-DEC-2000; 2000WO-US34998.
XX 23-DEC-1999; 99US-0171622.
XX (COR-) COR THERAPEUTICS INC.
XX Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;
XX Holloperter G;
XX WPI: 2001-418082/44.
XX DR N-PSDB; AAD08700.
XX
XX Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful
XX for identifying binding partners and for diagnostic applications -
XX
XX Claim 29; Page 91-92; 108pp; English.
XX
XX The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed
XX as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is
XX the subtype of P2-purine receptor. The P2Y12 receptor is expressed
XX selectively in the platelets and brain, and couples to a pertussis toxin-
XX sensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor
XX that responds to ADP. The invention also relates to a method for
XX identifying an agent which is useful for modulating acute myocardial
XX infarction, unstable angina, chronic stable angina, transient ischemic
XX attacks, strokes, peripheral vascular disease, preclampsia, deep venous
XX thrombosis, embolism, disseminated intravascular coagulation, thrombotic
XX thrombocytopenic purpura or a bleeding disorder; thrombotic and
XX restenotic complications following angioplasty, carotid endarterectomy,
XX post CABG (coronary artery bypass graft) surgery, vascular graft surgery,
XX stent placements or insertion of endovascular devices and prostheses.
XX P2Y12 receptor is useful for identifying binding partners and for
XX diagnostic applications. P2Y12 receptor provides targets for screening
XX compound libraries to regulate platelet aggregation, vascular injury, or
XX disease as well as schizoprenia, eating disorders, depression, migraine
XX and other brain disorders. The present sequence is human P2-purine
XX receptor subtype, P2Y12 truncated allelic variant. The variant is
XX obtained by deleting two bases 'CA' from position 789-790 of the wildtype
XX human P2Y12 receptor cDNA, resulting in amino acid changes from position
XX 240 of the wildtype human P2Y12 receptor.
XX
XX Sequence 267 AA:
SO

Query Match 69.6%; Score 1237.5; DB 22; Length 267;
Best Local Similarity 95.7%; Pred. No. 9.4e-128;
Matches 242; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

This Page Blank (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2002, 15:28:52 ; Search time 17.7 Seconds
(without alignments)
1856.641 Million cell updates/sec

Title: US-09-827-937a-2

Perfect score: 1778

Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SQDNRRKKEDGGDPNETPM 342

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR-71:*
1: pirl:*
2: pirl:*
3: pirl:*
4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	394	22.2	342	2 A40191	platelet-activatin
2	392.5	22.1	342	2 S13638	platelet-activatin
3	379.5	21.3	361	2 B45680	G protein-coupled
4	366	20.6	341	2 S63666	platelet-activatin
5	362	20.4	341	2 S43252	platelet-activatin
6	357.5	20.1	308	2 I50241	G protein-coupled
7	339	19.1	359	2 S15403	angiotensin II rec
8	338	19.0	344	2 T09508	intron 17 putineg
9	329	18.5	359	2 I39418	angiotensin II rec
10	326	18.3	359	2 S44425	angiotensin II rec
11	325.5	18.3	359	2 I48705	proteinase activat
12	325	18.3	359	2 A48857	angiotensin II rec
13	321	18.1	359	2 JCI104	angiotensin II rec
14	321	18.1	370	2 JCS549	heptahelical P215-
15	319	17.9	359	2 A42656	angiotensin II rec
16	318	17.9	359	2 JCI194	angiotensin II rec
17	318	17.9	359	2 JCI194	angiotensin II rec
18	318	17.9	359	2 JH0621	angiotensin II rec
19	317.5	17.9	365	2 S68208	G protein-coupled
20	317.5	17.9	365	2 S68208	mu oploid receptor
21	314.5	17.7	398	2 I56504	mu oploid receptor
22	314	17.7	359	2 JCI1516	angiotensin II rec
23	313.5	17.6	380	2 I38453	angiotensin recept
24	310.5	17.5	362	2 JN0694	angiotensin II rec
25	309	17.4	392	2 S65633	opioid receptor mu
26	309	17.4	400	2 I56533	mu opiate receptor
27	306	17.2	397	2 S66518	proteinase-activat
28	304.5	17.1	398	2 A57510	mu oploid receptor
29	299	16.8	380	2 JCI2434	kappa oploid recep

30	298.5	16.8	365	2 S68679	G protein-coupled
31	298	16.8	380	2 A48227	kappa oploid recep
32	297.5	16.7	359	2 I51372	angiotensin II rec
33	297.5	16.7	360	2 A53611	interleukin-8 rece
34	297	16.7	380	2 A55259	kappa oploid recep
35	296.5	16.7	420	2 I51667	thrombin receptor
36	296	16.6	380	2 S36143	kappa oploid recep
37	295	16.6	380	2 JCI338	kappa oploid recep
38	292.5	16.5	362	2 S33733	G protein-coupled
39	291.5	16.4	373	2 A47556	ATP receptor P2u -
40	290.5	16.3	352	2 A45747	neuropeptide Y/pep
41	284.5	16.0	333	2 I38974	G protein-coupled
42	282.5	15.9	352	2 G00048	fusin (LESTRA) - c
43	282	15.9	352	2 A43113	chemokine (C-C) re
44	282	15.9	355	2 J01231	interleukin-8 rece
45	281.5	15.8	353	2 S28787	neuropeptide Y/pep

ALIGNMENTS

RESULT 1
A40191
platelet-activating factor receptor - human
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1992 #sequence, revision 28-Aug-1992 #extl, change 20-Jun-2000
C:Accession: A40191; JH0479; A41079; JCI359; A42831; I51923
R:Kunz, D.; Gerard, N.P.; Gerard, C.
J. Biol. Chem. 267, 9101-9106, 1992
A:Title: The human leukocyte platelet-activating factor receptor, cDNA cloning, cell
A:Reference number: A40191; MUID:92250505
A:Accession: A40191
A:Molecule type: mRNA
A:Residues: 1-342 <KUN>
A:Cross-references: GB:W6674; NID:9456293; PIDN:AAA60002.1; PID:9456294
R:Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochane, C.G.
Biochem. Biophys. Res. Commun. 180, 105-111, 1991
A:Title: Characterization of a human cDNA that encodes a functional receptor for plat
A:Reference number: JH0479; MUID:92028922
A:Accession: JH0479
A:Molecule type: mRNA
A:Residues: 1-342 <YE>
A:Cross-references: GB:M80436; NID:9189537; PIDN:AAA60001.1; PID:9189538
A:Experimental source: GB:granulocyte, cell line HL-60 all
R:Nakamura, M.; Honda, Z.; Izumi, T.; Sekanaka, C.; Mutoh, H.; Minami, M.; Bito, H.;
J. Biol. Chem. 266, 20400-20405, 1991
A:Title: Molecular cloning and expression of platelet-activating factor receptor from
A:Reference number: A41079; MUID:92041873
A:Accession: A41079
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-342 <NAK>
A:Cross-references: GB:DI0202; GB:D90433; NID:9219975; PIDN:BAA01050.1; PID:9219976
R:Sugimoto, T.; Tsuchimochi, H.; McCreight, C.G.A.; Mutoh, H.; Shimizu, T.; Kurachi, Y
Biochem. Biophys. Res. Commun. 189, 617-624, 1992
A:Title: Molecular cloning and characterization of the platelet-activating factor rec
A:Reference number: JCI359; MUID:93112021
A:Accession: JCI359
A:Molecule type: mRNA
A:Residues: 1-315, 'N', 317-342 <SUG>
A:Experimental source: heart
A:Note: the authors translated the codon AAT for residue 316 as Lys
R:Sejritied, C.E.; Schweickart, V.L.; Godiška, R.; Gray, P.W.
Genomics 13, 832-834, 1992
A:Title: The human platelet-activating factor receptor gene (PTAFR) contains no intro
A:Reference number: A42831; MUID:92347886
A:Accession: A42831
A:Molecule type: DNA
A:Residues: 1-226, 'TG', 229-342 <SEY>
A:Cross-references: GB:M88177; NID:9190697; PIDN:AAA60214.1; PID:9190698
A:Note: sequence extracted from NCBI backbone (NCBIN:109813, NCBIIP:109814)
R:Chase, P.B.; Halonen, M.; Regan, J.W.
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993

A:Title: Cloning of a human platelet-activating factor receptor gene: evidence for an 11.1 kb gene
A:Reference number: 151923; MUID:93192035
A:Accession: 151923
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-342 <RES>
A:Cross-References: GB:S56396; NID:q298580; PIDN:AA625755.1; PID:q298581
C:Genetics:
C:Gene: GDB:PTAFR
A:Cross-References: GDB:128806; OMIM:173393
A:Map position: 1p35-1p34.3
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; transmembrane protein
F:17-38/Domain: transmembrane #status predicted <TRI>
F:54-75/Domain: transmembrane #status predicted <TRI>
F:92-113/Domain: transmembrane #status predicted <TRI>
F:134-155/Domain: transmembrane #status predicted <TRI>
F:184-205/Domain: transmembrane #status predicted <TRI>
F:233-253/Domain: transmembrane #status predicted <TRI>
F:277-297/Domain: transmembrane #status predicted <TRI>

Query Match	22.2%	Score 394;	DB 2;	Length 342;
Best Local Similarity	32.6%	Pred. NO. 1.6e-26;		
Matches 107; Conservative	61;	Mismatches 134;	Indels 26;	Gaps 10;

[illegible]

RESULT 2
S13638
platelet-activating factor receptor - guinea pig
C:Species: *Cavia porcellus* (guinea pig)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 08-Oct-1999
C:Accession: S13638
R:Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.; T
Nature 349, 342-346, 1991
A:Title: Cloning by functional expression of platelet-activating factor receptor from gu
A:Reference number: S13638; MUID:91101726
A:Accession: S13638
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-342 <HON>
A:Cross-references: GB:X56736; NID:g49442; PIDN:CAA0060.1; PID:g49443
A:Note: The species of guinea pig is not identified; In Genbank entry CCPAFREC, release
A:Superfamily: ATP receptor p2u

Query Match	22.1%;	Score 392.5;	DB 2;	Length 342;
Best Local Similarity	30.7%;	Pred. No. 2.1e-26;		
Matches 103;	Conservative 66;	Mismatches 146;	Indels 21;	Gaps 9;

```

0Y  DRYKIVQVEPLLYVAVFVGLITNGLARIFQFI--RKSXFI--IFLKNYISOLLMI 76
10  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y  20  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  10  DSEFYITLFPYIYIITFLGIIANGVYLVAFARLYPSKSKLNEIKIFMNVLTADLEIT 69
0Y  77  FPFKLSDPAKIGTGDLRFVCQVTSVLYFFPMYISISFLGLITIDRQKTRTPKTSNPK 136
Db  70  IFLMIVYVYSSNOGNMFLPKEFLCNLNGCFEINTYCSVAFGLIYITNRQAVKPYIKTQAT 129
0Y  137  NLLGAKITSVYIW-----AFMFLSLPRLMILTNPQROBRKNKCSFLKSEFG----LVMH 187
Db  130  TKRGKIALSLVYIWAIVAASVFLYMDSTNVNKKAGSGNITRC--FEHYEKGSKVLIIH 188
0Y  168  ELVANIICQYI--FWINELIYIYCYLILIKELYRSYVTRRGVAKYPRKRVANKVFLIIAVF 246
Db  189  ----TCLVIGFEYFELLILFCNLVIITHTLROPKQORNAEV--RRRLMNVCTVLAVFV 242
0Y  247  ICEVHFHARIPYTLISQTRDFDCETAENTLELYVEKSTLMLTSLNACDPEYFLFKSFR 306
Db  243  ICEVHHNVOLPWTLAEL--GMWPSNHOAINDAHQVTLCLSTKCDLPVYICFLTKKR 301
0Y  307  NSLIJMLKCPNSATLSODNKKKKEDGDGDPNEHPEM 342
Db  302  KHLSEKLNIMRSSOKCSRYTTDTGETEAMIPINHTPV 337

```

RESULT 3
B45680
G:protein-coupled peptide receptor EBI 2 - human
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: B45680
R:Birkenbach, M.; Josefsen, K.; Valamanchi, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A:Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled
A:Reference number: A45680, MUID:93186173
A:Accession: B45680
A:Status: Preliminary
A:Molecule type: nucleic acid
A:Residues: 1-361 <BIR>
A:Cross-references: GB:L08177; NID:g9292056; PID:AAA3924.1; PID:g9292057
A:Experimental source: B:lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBIN:127096, NCBIPI:127097)
C:Keywords: G protein-coupled receptor; transmembrane protein

```

Query Match          21.3%: Score 379.5; DB 2; Length 361.
Best Local Similarity 26.0%: Pred. No. 3e-25;
Matches   94; Conservative    84; Mismatches 152; Indels   31; Gaps   11.

OY      1 MOAVNLNT----SAGGNLSLCTRDYKINQVLPPLLYTVLFEPGLITNGIAMRIEFOIRSK 56
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      3 IOMANNFTPPSPATPGONCDCLYAHHSSTARIVAPLAHSLVEFIIIGLVGNLTALVIYIQRKK 62

OY      57 SN-FIFLEKNYISDLMLTLMITEPFRL-----SDAKLGTPRTFYCQVTSVFETMYI 110
       ||::||::||||::||::||::||::||::||::||::||::||::||::||
Db      63 INSTLLYSINLYISDILFTTLPTAIAYAMGFDRIGDA-----LCRTTALVFIIINTYA 117

OY      111 SISFGILTIDRYOKTTREPKTSNKRNLGAKILSVIAWAEFMFLSLPMNI--LTNRQPR 168
       :::::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      118 GVNFMTCLSIDPFIANVHPRLRYNKIKRRIEHAGCVLFWIILVFAQTLPILLIMPMSKEWE 177

OY      169 DKNVAKCSFLKSEFGLVWHEIIVNYTCQVILEWINFPIIVICYTLITKEILRS-----YYFT 223
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      178 RITCEMEYRPFEEETKSIPM--ILLGACFIGYVLPLIIIIILCYSQIOCKLETAKQNPLPEX 235

OY      224 RGCVGVPRKKRVAVKVFIIIAVEFCFVPBEHARIDYTLSQTR--DYEDCTAENTLFEYKE 281
       ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      236 SCVNK---KALNT-IILIIVFVLCTFPYVAHAIQHMIKRLRFNSNFLCEQSRRHSPOISLH 291

OY      282 SLIMLTSLNACLDPITYFFELCKSFENSLSIKCPENSATSLSDNNRKKEODGGDPNEETP 341
       |::||::||::|||||||::||::||::||::||::||::||::||::||::||

```


Db 292 FTVCGLMNCMDPFIYFACKGKRRKVMMLK-RQVSVSISAVKSAPENSKEMTETQ 350

Qy 342 M 342

Db 351 M 351

RESULT 4

S6366

platelet activating factor receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C:Accession: S63666

R:Smith, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.

Biochem. J. 314, 671-678, 1996

A:Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localization

A:Reference number: S63666; MUID:96239129

A:Accession: S63666

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 <ISH>

A:Cross-references: EMBL:DS0872; NID:91256924; PIDN:BAA09468.1; PID:91256925

C:Superfamily: ATP receptor P2u

Query Match 20.6%; Score 366; DB 2; Length 341;

Best Local Similarity 29.9%; Pred. No. 4.1e-24;

Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;

Qy 20 DYKIQVLPFLYTVLFFVGLITNGLAMRIEFOI--RSKSNFI-IFLKNVTSIDLMLIT 76

10 DSEFRYTLFPIYSVIFILGVANGVYLVWFANLPSKRLNEIKIFMVLTMADLLFLIT 69

Qy 77 FPFKLSDAKLGTPGRFVQCVTSVIFETMYSISFLGLITDRYQKTRPFTSNPK 136

70 LPLMIVVYNSNEGDWILPFLCNVACLFINTYCSVAFGVITNNKQVAVPIKTAQAT 129

Db 137 NLGAKISVIVAFM-----FLSLPMILITNROPDRKNVKSFLKSEFG--LYWHE 188

130 TRKRGISLTIWISIVATASFYLATDSNVLNPKDGSNITRCHEHYEPYVPLIVAV 189

Qy 189 IVNYICQVIFWIFLI-VIVCYTLTKELYSVTRGVGKVPKKVNVKVIIVAFPI 247

190 FIACFEFLFIFVCNLIIVITLLQPMROO--RKAGV----KRRALMVCVTLAVFI 243

Qy 248 CVPPFPAIPTLSQTRVDVDCIAENTLEFYKESFLMTLSNACDPIYFLCKSPFN 307

244 CVPVHVQVLPMTLAEIG--YQTFHQAIINDAHQITLCLLSTNCVLDPIYICFLTKPKR 301

Qy 308 -----SLISMLKCPNSATS 321

302 HLESEKYSMRSSKRC-SRATS 321

RESULT 5

S43252

platelet-activating factor receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999

C:Accession: S43252

R:Blito, H.; Honda, Z.; Nakamura, M.; Shimizu, T.

Eur. J. Biochem. 221, 211-218, 1994

A:Title: Cloning, expression and tissue distribution of rat platelet-activating-factor-T

A:Reference number: S43252; MUID:94222063

A:Accession: S43252

A:Molecule type: mRNA

A:Residues: 1-341 <RNT>

A:Cross-references: GB:004740; NID:9470384; PIDN:AAA18422.1; PID:9470385

C:Superfamily: ATP receptor P2u

Query Match 20.4%; Score 362; DB 2; Length 341;

Best Local Similarity 28.9%; Pred. No. 9e-24;

Matches 96; Conservative 66; Mismatches 120; Indels 50; Gaps 10;

Qy 20 DYKIQVLPFLYTVLFFVGLITNGLAMRIEFOI--RSKSNFI-IFLKNVTSIDLMLIT 76

10 DSEFRYTLFPIYSVIFILGVANGVYLVWFANLPSKRLNEIKIFMVLTMADLLFLIT 69

Qy 77 FPFKLSDAKLGTPGRFVQCVTSVIFETMYSISFLGLITDRYQKTRPFTSNPK 136

70 LPLMIVVYNSNEGDWILPFLCNVACLFINTYCSVAFGVITNNKQVAVPIKTAQAT 129

Qy 137 NLGAKISVIVAFM-----FLSLPMILITNROPDRKNVKSFLKSEFG--LYWHE 188

130 TRKRGISLTIWISIVATASFYLATDSNVLNPKDGSNITRCHEHYEPYVPLIVAV 189

Qy 177 FLKSEFGLVMEIYNYICQVIFWIFLI-VIVCYTLTKELYSVTRGVGKVPKKVNV 236

190 FITSCFVLFF-----LFYCNMVI--HLLTRP-----VROQRKEVRRALMM 233

Qy 237 KVFIIIAVFICVPEHFAPIPTLSQTRVDVDCIAENTLEFYKESFLMTLSNACDPI 296

234 -CVTVLAEVVICFVPHVQVLPMTLAEIG--YQTFHQAIINDAHQITLCLLSTNCVLDPI 290

Qy 297 IYFELCKSPFN-----SLISMLKCPNSATS 321

291 IYFLTKKFRKHLSEKYSMRSSKRC-SRATS 321

RESULT 6

150241

G protein-coupled receptor 6H1 - chicken

N:Alternate names: purinoceptor 6H1

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Jun-2000

C:Accession: I50241; JC4618

R:Kaplan, M.H.; Smith, D.I.; Sundick, R.S.

J. Immunol. 151, 628-636, 1993

A:Title: Identification of a G protein coupled receptor induced in activated T cells.

A:Reference number: I50241; MUID:93329058

A:Accession: I50241

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Cross-references: GB:I06109; NID:9304383; PIDN:AAB06587.1; PID:9304384

R:Webb, T.E.; Kaplan, M.G.; Barnard, E.A.

Biochem. Biophys. Res. Commun. 219, 105-110, 1996

A:Title: Identification of 6H1 as a p2y purinoceptor: p2y5.

A:Reference number: JC4618; MUID:96190677

A:Accession: JC4618

A:Molecule type: mRNA

A:Residues: 1-308 <WEB>

A:Cross-references: GB:L06109; NID:9304383; PIDN:AAB06587.1; PID:9304384

A:Experimental source: T-cells

C:Comment: This receptor plays a role in T-cell activation.

C:Genetics:

A:Gene: p2y5

C:Superfamily: ATP receptor P2u

C:Keywords: G protein coupled receptor; transmembrane protein

F:15-40/Domain: transmembrane #status predicted <TM1>

F:51-74/Domain: transmembrane #status predicted <TM2>

F:89-109/Domain: transmembrane #status predicted <TM3>

F:133-153/Domain: transmembrane #status predicted <TM4>

F:177-201/Domain: transmembrane #status predicted <TM5>

F:227-248/Domain: transmembrane #status predicted <TM6>

F:269-292/Domain: transmembrane #status predicted <TM7>

Query Match 20.1%; Score 357.5; DB 2; Length 308;

Best Local Similarity 29.5%; Pred. No. 2e-23;

Matches 87; Conservative 68; Mismatches 125; Indels 15; Gaps 8;

Qy 14 TSLCTRYKITQVLPFLYTVLFFVGLITNGLAMRIEFOI--RSKSNFI-IFLKNVTSIDL 72

3 SSNCSTEDSEKRYTLVGYGVSMVFVGLIANGCAVLIYFTFLKVNNETTTMLNLAIISDL 62

RESULT 7
S15403
angiotensin II receptor type 1 - bovine
C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1996
C:Accession: S15403
R:Sasaki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda, Y.
Nature 351, 230-233, 1991
A>Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angiotensin
A:Reference number: S15403; MUID:S1251900
A:Accession: S15403
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <SAS>
A:Cross-references: GB:X62294; NID:g43; PIDN:CAA44182.1; PID:g44
C:Superfamily: vertebrate rhodopsin

Query Match	19.1%	Score 339	DB 2	Length 359
Best Local Similarity	27.9%	Pred. No. 9.2e-22		
Matches	95	Conservative	62	Mismatches 143; Indels 40; Gaps 10;
QY	26	VLEPLLYLVLEFVGAGITNGL-AMRIEFOIQRKSNFIPLKNIIVISDLMLITFEPKRIISD	84	
	::	::	::	::
Db	29	IMIPFLYSIIIFVVGLEFGNSLVVIVYIFPKKLTVASVFLNLALDLCFLLLPLIMAYYT	88	
QY	85	AKLGTGPLETEVCQVTSVYIEFTMYISISFLGLITIDRYOKTTREPKSNPKNLGAKIL	144	
	::	::	::	::
Db	89	AMEYKMPGNYLCKITASASVSEFNLAASVFLTLCTSIDRLAIVHMKSLRRTMLVAVYT	148	
QY	145	SVVIAFAFELLISLPMILTN-RQPRDKVVKCSF-----LKSEFGLVHEIYNYICQ	195	
	::	::	::	::
Db	149	CIITMLGLASLPITIIHRNVEFIENTNITCAFYESONSNTLPVGLGLT-KNIGFL--	205	
QY	196	VIFWFLNIVIVCYLLIRKLEYRSVYRTRGVKKRVKNVKEIIIAVFICFPRFHA	255	
	::	::	::	::
Db	206	---FPFLIITSLTLMKLTLLKAEIOK---NKRPRKIDIKIILAIIVLFFP-----FS	252	
QY	256	RIPPTLSQTRVY-----DCTAENTLEYVKESTLMLTSLNACIDPEIYFELCKSEFNS	308	
	::	::	::	::
Db	253	WVPHQIETFMGVLLIOLGLIRIDCKIEDIYDVTAMPTICICLAYFNNCNPLFVYFLGKKFKKY	312	
QY	309	LISMUK-CPNSATSLSQDNRK-----KEODGQDPNETP	341	
	::	::	::	::
Db	313	FLQILKTYIPPKAKSHSNLSTMASTLSTYRPSNGNSSTKRP	352	

RESULT 8
T09508
intron 17 purinergic receptor P2Y5 - human
N:Alternate names: G-protein coupled receptor
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999
C:Accession: T09508
R:Bohm, S.K.; Trump, A.; Khitlin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-344 <BOH>
A:Cross-references: EMBL:AF000546; NID:g2232068; PID:g232069
C:Genetics:
A:Map position: 13
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; transmembrane protein

[illegible]

RESULT 9
I39418
angiotensin II receptor type 1b - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 24-Nov-1999
C:Accession: I39418
R:Kuroda, S.
Biochem. Biophys. Res. Commun. 199, 467-474, 1994
A:Title: Novel subtype of human angiotensin II type 1 receptor: cDNA cloning and expression
A:Reference number: I39418; MUID:94183213
A:Accession: I39418
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <RES>
A:Cross-references: GB:J13814; NID:g471120; PIDN:BA02968.1; PID:g471121
Superfamily: vertebrate rhodopsin

[illegible]

```

Oy 145 SVVIAEFMFLSTENMILT-N-RDPDRKNVKGCF-----LKSEGLWHEIYVITQ 195
Db 149 CIITMLAGLASLPAITHRNVFLENTNITVCAPHHESRNSITPLIGLGLKNTLGS -C- 205
Oy 196 VIFMINEFLIVCYTLTKTELKYSYVTRCGVAPRKVKVVFIIIAVEFICFVPHFA 255
Db 206 ----FPFIIITSTLTMLKMLKKAYEQK---NNPRNDIOFRIMAVLVEFF-----FS 252
Oy 256 RIPTLSQTRDYV-----DCTAENTLFYVKSESTMLTSLNACDLPFYFLCKSFNRS 308
Db 253 WIPQIETFDLVLLIQGIIIRDCRIADIVDPAMPTITWIAVFNNCENLDPFYEGFGKKKKD 312
Oy 309 LISMLK-CPNASATLSQDNKR 328
Db 313 ILQLLKTYIPPKAKSHSNLSTK 333

```

RESULT 10
S44425
angiotensin II receptor type 1 - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S44425
R:Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.
FEBS Lett. 343, 146-150, 1994
A:Title: Molecular cloning of the canine angiotensin II receptor. An AT1-like receptor v
A:Reference number: S44425; MUID:94222188
A:Accession: S44425
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-359 <BUR>
A:Cross-references: PIDN:AAB30674.1; PID:g546569
A:Experimental source: liver
C:Superfamily: vertebrate rhodopsin

```

Query Match      18.3% Score 326; DB 2; Length 359;
Best Local Similarity 29.2%; Pred. No.1.2e-20;
Matches 92; Conservative 54; Mismatches 147; Indels 22; Gaps 1
QY 26 VLFPLLVTLVEFVGLITNGL-AMRIFFQIRSKSNFIIFLKNVILSDMLILTFPEFKILD 84
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 29 VMIPFLYSIIIFVNGIFGSLVIVYIYFWMKLTQVASFLLNLNLADCLCLTLPMAVYT 88
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 85 AKLGTPRTVFCOVTSYIYFTMTYISISFLGTLIDRYQKTRTPPKTSNPKNLGAKTL 144
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 89 AMEYRMPEGNLYCKTASASVSFNLTASVFLTLCLSIDRVAIVHMPKSVRRRTMLMAKYT 148
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 145 SVVIMAFNFFLSTLPMILTN-RQPRDKNKKKSF-----LKSEGLVMEHIVNYICO 195
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 149 CIIIVLGLAGLASLPPIIHRNVEFIENNTIYCAFIYESONSTLPIGLGTL-KNLTGFL-- 205
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 196 VIFWFLNFIIVACYTLIRKELRYSVARTRGVGVBRKKKNVAVFI-IIVFICFVPFHF 254
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 206 ----PPFLIILTSYTLIKMKTAKRAIEIQ---NKRNDIDFIIIMAIYVLEFFFSWVPHOI 258
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 255 ARIPTYSQTRDVEDCTAENLTLEYVKESTLWLTSLINACIDPEIYFFELCKSPRNSLSIMUK 314
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 259 FTFLDVLVQLQGIHHCCKIADIIVDTAMPITICIAVENNCINLPFLGYGLGKFKFYQLQLLK 318
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 315 -CPNSATSLSDNKR 328
Db 319 YIPPAKSHSSLSLK 333

```

RESULT 11
I48705
proteinase activated receptor 2 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_rev1sion 02-Jul-1996 #text_change 24-Nov-1996
C:Accession: I48705
R:Myrstedt, S.; Larsson, A.K.; Aberg, H.; Sundelin, J.
J. Biol. Chem. 270, 5950-5955, 1995

A:Title: The mouse proteinase-activated receptor-2 cDNA and gene. Molecular cloning a
A:Reference number: I48705; MUID:95197620
A:Accession: I48705
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-399 <RES>
A:Cross-references: EMBL:Z48043; NID:g663020; PIDD:CA88097.1; PID:g663021
C:Superfamily: ATP receptor P2u

[illegible][illegible]

Job time: 130 sec

Db 194 KRWKTYLSKTTFFIEVVGFIPLILNVSCSSVLRRLRKPATLSQIGTN-----KKRV 247
QY 235 NVKVFIIIAVEFICFPFHPARIPYTLSDTRDVPDCAENTLFFVKESTLMTLSINACLD 294
Db 248 LKMTVMAVFCVFCFVYNSLVFLKALVRSQAITNCFLEFAKIMYPITLCIATLNCQFD 307
QY 295 PFIFYFLCKSFRRNS 308
Db 308 PFIFYFLCKSFRRNS 321

RESULT 15

A42636
angiotensin II receptor type 1B (AT3) - rat
N:Alternate names: angiotensin II receptor chain B
C:Species: Rattus norvegicus (Norway rat)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A42656; S20423
R:Sandberg, K.; Ji, H.; Clark, A.J.; Shapiro, H.; Catt, K.J.
J. Biol. Chem. 267, 9455-9458, 1992
A:Title: Cloning and expression of a novel angiotensin II receptor subtype.
A:Reference number: A42656; PMID:92250585
A:Accession: A42656
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <SAN>
A:Cross-references: GB:M90065; NID:g202801; PIDN:AAA40704.1; PID:g202802
A:Experimental source: adrenal cortex
A>Note: sequence extracted from NCBI backbone (NCBIN:100262, NCBI:P:100268)
R:Wai, N.; Inagami, T.
FEBS Lett. 298, 257-260, 1992
A:Title: Identification of two subtypes in the rat type I angiotensin II receptor.
A:Reference number: S20423; PMID:92183879
A:Accession: S20423
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-359 <IWA>
A:Cross-references: GB:X64052; NID:g57521; PIDN:CAA45410.1; PID:g57522
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 17.9%; Score 319; DB 2; Length 359;
Best Local Similarity 29.6%; Pred. No. 4.9e-20;
Matches 92; Conservative 54; Mismatches 137; Indels 28; Gaps 10;

QY 26 VLFPLLTYVLFYGLITNGL-AMRIFQIRKSNFIIFLKNTVISDLMILTFPKILSD 84
Db 29 VMPTLTSILFVVGIFGNSLVIVIFYMKLTIVASVFLNLALADLCFLTLPLMAVYT 88
QY 85 AKGTGFLRTFVCOVTVIFYFTWYISIFLGTITDRYOKTTRPFKTSNPKNLGAKIL 144
Db 89 AMEYRMPFGNHLCKIASASVFNLYASVFLTCLSIDRYLAIVHPMSRLRRTMLVAKYT 148
QY 145 SVVIMAFMFLSLPNMILTNRQ-PRDRNVKRCSE-----LKSEGLVWHEIVNYICQ 195
Db 149 CIITWLAGLASLPAYIVRVNYFIENNTIVCAHYESQNSTLPIGLGT-KNIGFY--205
QY 196 VIFMINFLIVCYTLTKTELRSYVTRGVGKYPKKVNVKVF-IITAV--PFICFV 251
Db 206 ----FPFLITLSTYLLMKALKAKYIKQ---NTPR--NDIFRIIMAVILVFFFSWVP 255
QY 252 FHFARIPYTLSDTRDVPDCAENTLFFVKESTLMTLSINACLDPFIFYFLCKSFRRNSLIS 311
Db 256 HQFTFLDVLIQGLINDCEIADIVDAMPITICIAVFNCLNPLFYGLGKKKKRYFLQ 315
QY 312 MLK-CPNSATS 321
Db 316 LKTYIPTAKS 326

Search completed: September 6, 2002, 15:31:02

This Page Blank (uspt~,

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: September 6, 2002, 15:30:42 : Search time 13.4 Seconds

(without alignments)
988.215 Million cell updates/sec

Title: US-09-827-937A-2

Perfect score: 1778

Sequence: 1 MQAVDNLTSAGCNTSLCTRD.....SODNRKKEDGSDPNEETPM 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	772	43.4	338	1 K101_HUMAN	Q15391 homo sapien.
2	694	39.0	305	1 K101_RAT	Q35881 ratius norv
3	488	27.4	319	1 H963_HUMAN	Q14626 homo sapien
4	411.5	23.1	375	1 GPRX_MOUSE	Q91166 homo muscicu
5	409.5	23.0	381	1 GPRX_HUMAN	Q91065 homo sapien
6	394	22.2	342	1 PAFR_HUMAN	P25105 homo sapien
7	392.5	22.1	342	1 PAFR_CAVPO	P21536 cavia porce
8	379.5	21.3	361	1 EBIT2_HUMAN	P32249 homo sapien
9	367	20.6	345	1 CLT2_PIG	Q35003 sus scrofa
10	366	20.6	341	1 PAFR_MOUSE	Q62035 mus muscicu
11	362	20.4	341	1 PAFR_RAT	P46002 ratius norv
12	357.5	20.1	308	1 P215_CHICK	P32250 gallus gall
13	347.5	19.5	346	1 CLT2_HUMAN	Q35075 homo sapien
14	347.5	19.5	337	1 P215_XENLA	P79928 xenopus lae
15	344	19.3	309	1 CLT2_MOUSE	Q32061 mus muscicu
16	339.5	19.1	359	1 CLT2_RAT	Q92419 ratius norv
17	339	19.1	359	1 AG2R_BOVIN	P25104 bos taurus
18	338	19.0	344	1 P215_HUMAN	P43657 homo sapien
19	334	18.8	359	1 AG2R_SHEEP	O77590 ovis aries
20	329.5	18.5	359	1 GPRH_HUMAN	Q13304 homo sapien
21	329	18.5	359	1 GPRH_HUMAN	Q13725 homo sapien
22	328	18.4	340	1 CLT1_PIG	Q35055 sus scrofa
23	327	18.4	359	1 AG2R_PIG	P30555 sus scrofa
24	326	18.3	359	1 AG2R_CANFA	P43240 canis fami
25	325.5	18.3	359	1 PAR2_MOUSE	P35086 mus muscicu
26	325	18.3	359	1 AG2R_RABIT	P49766 oryctolagus
27	321	18.1	359	1 AG2R_HUMAN	P30556 homo sapien
28	320	18.0	359	1 AG2R_CAVPO	Q91166 cavia porce
29	320	18.0	370	1 P215_HUMAN	Q99677 homo sapien
30	319.5	18.0	365	1 GPR8_HUMAN	Q15743 homo sapien
31	319	17.9	359	1 AG2R_RAT	P25095 ratius norv
32	319	17.9	359	1 AG2S_RAT	P29089 ratius norv
33	318	17.9	359	1 AG2R_MOUSE	P29754 mus muscicu

34	316.5	17.8	398	1 OPRM_RAT	P33535 ratius norv
35	316	17.8	359	1 AG2S_MOUSE	P29755 mus muscicu
36	316	17.8	377	1 AP2_RAT	Q91063 ratius norv
37	316	17.8	397	1 PAR2_RAT	Q63645 ratius norv
38	313.5	17.6	380	1 AP2_HUMAN	P33414 homo sapien
39	313.5	17.6	401	1 OPRM_PIG	Q95247 sus scrofa
40	312	17.5	359	1 AG2R_BOVIN	Q35210 meriones un
41	312	17.5	401	1 OPRM_BOVIN	P79350 bos taurus
42	311	17.5	369	1 PAR3_MOUSE	Q08675 mus muscicu
43	310.5	17.5	362	1 AG2R_XENLA	P32303 xenopus lae
44	310.5	17.5	363	1 AG2S_XENLA	P35373 xenopus lae
45	310	17.4	374	1 PAR3_HUMAN	Q00254 homo sapien

ALIGNMENTS

RESULT	ID	Accession	Standard	PRT	338 AA
1	K101_HUMAN	Q15391	STANDARD	PRT	338 AA
AC	15-JUL-1998	(Rel. 36, Created)			
DT	15-JUL-1998	(Rel. 36, Last sequence update)			
DT	30-MAY-2000	(Rel. 39, Last annotation update)			
DE	Probable G protein-coupled receptor KIAA0001.				
GN	KIAA0001.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Bone marrow;				
RX	MEDLINE=96051387; PubMed=7584026;				
RA	Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,				
RA	Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;				
RT	"Prediction of the coding sequences of unidentified human genes. I.				
RT	The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by				
RT	analysis of randomly sampled cDNA clones from human immature myeloid				
RT	cell line KG-1."				
RL	DNA Res. 1:27-35(1994).				
CC	-1- FUNCTION: ORPHAN RECEPTOR.				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@sib-sib.ch).				
CC	-----				
CC	EMBL: D13626; BAA02791.1; .				
DR	GCRDB: GCR 0594; .				
DR	InterPro: IPR000276; GPCR_Rhodpsn.				
DR	Plan: PF00001; 7tm_1; 1.				
DR	PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; FALSE_NEG.				
DR	PROSITE: PS00262; G_PROTEIN_RECPT_F1_2; 1.				
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.				
FT	DOMAIN 1				
FT	TRANSMEM	30	50	1 (POTENTIAL)	
FT	DOMAIN	51	55	1 (POTENTIAL)	
FT	TRANSMEM	56	76	2 (POTENTIAL)	
FT	DOMAIN	77	96	EXTRACELLULAR (POTENTIAL)	
FT	TRANSMEM	97	117	3 (POTENTIAL)	
FT	TRANSMEM	118	139	4 (POTENTIAL)	
FT	TRANSMEM	140	160	4 (POTENTIAL)	
FT	DOMAIN	161	188	EXTRACELLULAR (POTENTIAL)	
FT	TRANSMEM	189	209	5 (POTENTIAL)	
FT	DOMAIN	210	234	CYTOPLASMIC (POTENTIAL)	
FT	TRANSMEM	235	255	6 (POTENTIAL)	

between the Swiss Institute of Bioinformatics and the EMBL outstation - CC
CC This Swiss-Proj entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: AF002986; AAC51846.1; .
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR000237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 21
FT TRANSMEM 22 42
FT DOMAIN 43 48
FT TRANSMEM 49 69
FT DOMAIN 70 89
FT TRANSMEM 90 110
FT DOMAIN 111 132
FT TRANSMEM 133 153
FT DOMAIN 154 181
FT TRANSMEM 182 202
FT DOMAIN 203 224
FT TRANSMEM 225 245
FT DOMAIN 246 268
FT TRANSMEM 269 289
FT DOMAIN 290 319
FT CARBOHYD 3
SQ SEQUENCE 319 AA; 36754 MW; 79B9821C10841114 CRC64;

Query Match 27.4%; Score 488; DB 1; Length 319;
Best Local Similarity 34.5%; Pred. No. 3.2e-26; Mismatches 125; Indels 26; Gaps 9;

Matches 112; Conservative 62; Mismatches 125; Indels 26; Gaps 9;
QY 13 NPSLCRDYKITYVLPFLYLVFVGLITNGLAMRIFFOIRSKSNFI-IFLKNTVISDL 71
DB 3 NSSEFCPVYVDELP-FYFYYLVFVGLVIGSCFATMAFIQKNTNHRVCSTIYLNLITADF 61
QY 72 LMLTPPEFKLSDAKLGTP--LRTFVCQVTSVFYFTWISIFLGLITIDRYOKTRP 129
DB 62 LMLTLPAPVKIYVD--LGVAPMKLKIIFHCQVACLIYINMYLSIIFLAFVSIDRLQLTHS 119
QY 130 FKTSNPKNLGAKILSVIAFMFLSLPMNMLNRPORNVAKKCSLKEEFGVMEHI 189
DB 120 CKIYRIQEEFAMKISTVVLAVLWPMNMPITKIDIKESNVGCMEFKEFRNMHL 179
QY 190 VNYICQVIFWINE-LIVYVCYTLTKELYSYVTRGVGKVPK-KYVNVKFIILAAVEFI 247
DB 180 TNYICVAIF-LNFSAILLINCILVIRQLYRN---KDNENYNNKALINILLVTTGTGII 234
QY 248 CAVPFPFARIPYLSOTRDVCTAENTLFYVKESTLWLSLNLACDPFIYFLCKSEFN 307
DB 235 CFPVPHVIRIPYLSQTEVITDCSTRLSFKAKETALLAVSNLCFDPILYYHLSKAFRS 294
QY 308 SLI-----SMKCPNSA 319
DB 295 KYTEFASPKETAKOKEKLCENNA 319

RESULT 4
GPRY_MOUSE STANDARD; PRT; 375 AA.
AC Q9RIK6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable G protein-coupled receptor GPR34.
GN GPR34.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99326137; PubMed=10395919;
RA Schöneberg T., Schulz A., Grosse R., Schade R., Henkels P.,
RT Schöneberg T., Guderma T.,
RL "A novel subgroup of class I G-protein-coupled receptors.",
Biochem. Biophys. Acta 1446:57-70(1999).
CC - FUNCTION: ORPHAN RECEPTOR.
CC - SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC - TISSUE SPECIFICITY: BROADLY EXPRESSED.
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: AF081916; AAD50550.2; .
DR MGD: MGI:1346334; GPR34.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR000237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 54
FT TRANSMEM 55 75
FT DOMAIN 76 81
FT TRANSMEM 82 102
FT DOMAIN 103 121
FT TRANSMEM 122 142
FT DOMAIN 143 164
FT TRANSMEM 165 185
FT DOMAIN 186 209
FT TRANSMEM 210 230
FT DOMAIN 231 262
FT TRANSMEM 263 283
FT DOMAIN 284 303
FT TRANSMEM 304 324
FT DOMAIN 325 375
FT DISULF 120 197
FT CARBOHYD 21 21
FT CARBOHYD 29 29
FT CARBOHYD 35 35
FT CARBOHYD 193 193
FT CARBOHYD 288 288
SQ SEQUENCE 375 AA; 43173 MW; C04E1C1A52521045 CRC64;

Query Match 23.1%; Score 411.5; DB 1; Length 375;
Best Local Similarity 32.0%; Pred. No. 4.8e-21; Mismatches 154; Indels 9; Gaps 7;

Matches 101; Conservative 52; Mismatches 154; Indels 9; Gaps 7;
QY 2 QAVNLTSAFGNFSICTRDYKITOVLEPLLYLVFVGLITNGLAMRIFFOIRSKSNFI- 60
DB 25 QASQNSGVPNVTG-CPMDEKLSTVLTFTFYSVIFVGLVGNITALLYVFLGIRKNSIO 83
QY 61 IFLKNTVISDLMLITLFPKILSDAKLGCPGLRTFVCQVTSVFYFTWISIFLGLITI 120
DB 84 IYLLVAVADLLIFCLPRIMHINONKWTGVLGVKVGTLVNMWYISITLLPFTSL 143
QY 121 DRYOKTRPEFKTSNPKNLGAKILSVIAFMFLSLPMNMLNRPORNVAKKCSFLKS 180
DB 144 DRYIINNSIQGRRAITTKQSIYVCCIVWF-VALLGFLMILITLTKGGNINSMCHYRD 202
QY 161 EFGLVWHEIVNTICQVIFWINEFLIYVCYTLTKELR-SYVATR--GVGKVPKRVNKA 237
DB 203 RHNAAGEAIFNVLVWFWLILFLITLSYIKGNLRLTSKRSKPPNGKVPATYATARN-- 260

QY 238 VETIIAAVEICFVPHAFRIPYTTSQTSDVEDCCAEKNTLFVWKESTLMTSLNACLDPEI 297
|:::|:|||||:| | | | | :| | | | | :| | | | | :
Db 261 SFVIILITTCIFVPFHARFRFIYSQL-WSSCYWKELIHKTNEIMLVFSFNCLDPVM 319

QY 298 YEFICKSFRNLISML 313
||:|:|:|:|:
Db 320 YFLMSSNRKIKCOLL 335

RESULT 5
GPRY_HUMAN STANDARD; PRT; 381 AA.
ID GPRY_HUMAN
AC Q9UPC5; O95853;
DT 16-OCT-2001 (Rel. 40, Created)
DN 16-OCT-2001 (Rel. 40, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Probable G protein-coupled receptor GPR34.
GN GPR34.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=99326137; PubMed=10395919;
RA Schoneberg T., Schult A., Grosse R., Schade R., Henklein P.,
RT Schultz G., Gundermann T.;
RL "A novel subgroup of class I G-protein-coupled receptors.";
RN Biochim. Biophys. Acta 1446:57-70(1999).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99156852; PubMed=10036181;
RA Marchese A., Sawadogo M., Nguyen T., Cheng R., Heng H.H., Nowak T.,
RN Im D.-S., Lynch K.R., George S.R., O'Dowd B.F.;
RT "Discovery of three novel orphan G-protein-coupled receptors.";
RN Genomics 56:12-21(1999).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20434921; PubMed=10982042;
RA Jacobl F.K., Broghammer M., Pesch K., Zrenner E., Berger W.,
RN Mehlid R.A., Pusch C.M.;
RT "Physical mapping and exclusion of GPR34 as the causative gene for
RL congenital stationary night blindness type 1.";
RN Hum. Genet. 107:89-91(2000).
[4]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RN Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RN Arima M., Nabekura T., Ishii S., Kawai Y., Satoh K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y., Oshima A.;
RT "NEO human cDNA sequencing project";
RL Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.

- i- FUNCTION: ORPHAN RECEPTOR.
- i- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
- i- TISSUE SPECIFICITY: BROADLY EXPRESSED.
- i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/unannounce/>).
CC or send an email to license@isb-sib.ch.

DR EMBL; AF039686; AAD50531.1; -
DR EMBL; AF118670; AAD17248.1; -
DR EMBL; AK027780; BAB55362.1; -
DR MIM; 300241; -
DR InterPro; IPR000276; GPCR_Rhodpsn

DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; P800237; GPCRHHODPSN.
DR	PROSITE; PS00237; G_PROTEIN_RECEP_FL1; 1.
DR	PROSITE; PS50262; G_PROTEIN_RECEP_FL2; 1.
KW	Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein.
FT	DOMAIN 1
FT	TRANSMEM 62 82
FT	DOMAIN 88
FT	TRANSMEM 89 109
FT	DOMAIN 110 128
FT	TRANSMEM 129 149
FT	DOMAIN 150 171
FT	TRANSMEM 172 192
FT	DOMAIN 193 216
FT	TRANSMEM 217 237
FT	DOMAIN 238 269
FT	TRANSMEM 270 290
FT	DOMAIN 291 310
FT	TRANSMEM 311 331
FT	DOMAIN 332 381
FT	DISULFID 127 204
FT	CARBOHYD 28 28
FT	CARBOHYD 36 36
FT	CARBOHYD 42 42
FT	CARBOHYD 200 200
FT	CARBOHYD 295 295
FT	CONFLICT 181 181
SQ	SEQUENCE 381 AA; 43860 MW; 491FC0165624379 CRC64;

```

Query Match Similarity      23.0%; Score 409.5; DB 1; Length 381;
Best Local Similarity      32.3%; Pred. No. 6,7e-21;
Matches 102; Conservative 53; Mismatches 152; Indels 9; Gaps
7.

QY      2 QAVDMLTSPAGNTSLCTRDYKITQYLFLLYTVLEFFVGLITNGLAMRIFFQIRKSNFI - 60
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      32 GPQPNRSATP - NVTCPCMDERKLTSTVLTTYSVIFIVGLGNGIMIALYVFLGIRKRNSIO 90
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      61 FLKNTVIVSDLLMILFFPKILSDAKLGGLRTFVCOVTSVIAFFFWISISPLGINT 120
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      91 IYLLVNAIDLFLICPLPRIMVHINONKWTGVLICKVAGTFLFNMNITSIILGFI SL 150
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      121 DRYQKTTREPKTSNPKNLGAKILSVIAAFELSLPMMILNRPDRKNKCSFLKS 180
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      151 DRYIKINRISIQQRKAITTKQSIYOCIV - MLALGGFLMIIITLLKGGHNSMTCFHYRD 209
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      181 EGGLEWHELVANTICQVIFINFLIVACYTLLTKELXR - SYVRIR - GVGKVPKKVNVK 237
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      210 KINANGEALEFNILVYMEFLIFLLIILSYIKIGKNLIRSKRSKRPNSGKYATTAARN - 267
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      238 VETIIAVFICVPPHFARIPYTLSTQTRVFPCTAENTLFYVEKSTLWLTSLNACLDPEI 297
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      268 SEIVLIFPICVPHAFRFIYISQL - NVSSCYWKEIYHKNIEMILVLSFNSCLDPVM 326
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      298 YFFLCKSFRNLSLSML 313
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      327 YELSSNIRKIMCOLL 342
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT      6
PAFR_HUMAN  ID      PAFR_HUMAN      STANDARD:      PRT:      342 AA.
AC      P25105;
DT      01-MAY-1992 (rel. 22, Created)
DT      01-MAY-1992 (rel. 22, Last sequence update)
DT      16-OCT-2001 (rel. 40, Last annotation update)
DE      Platelet activating factor receptor (PAF-R).
GN      PAFR OR PAFR.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX      NCBI_TaxId=9606;
RN      [1]

```

RP SEQUENCE FROM N.A.
 RA MEDLINE-92028922; PubMed-16556963;
 RA Ye R.D., Prossnitz E.R., Zou A., Cochrane C.G.;
 RT "Characterization of a human cDNA that encodes a functional receptor
 RT for platelet activating factor.";
 RL Biochem. Biophys. Res. Commun. 180:105-111(1991).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE-92041873; PubMed-1657923;
 RA Nakamura M., Honda Z., Izumi T., Sakanaka C., Mutoh H., Minami M.,
 RA Bito H., Sawayama Y., Matsumoto T., Noma M., Shimizu T.;
 RT "Molecular cloning and expression of platelet-activating factor
 RT receptor from human leukocytes.";
 RL J. Biol. Chem. 266:20400-20405(1991).
 RN (3)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92250505; PubMed-1374385;
 RA Kunz D., Gerard N.P., Gerard C.;
 RT "The human leukocyte platelet-activating factor receptor. cDNA
 RT cloning, cell surface expression, and construction of a novel
 RT epitope-bearing analog.";
 RL J. Biol. Chem. 267:9101-9106(1992).
 RN (4)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92347886; PubMed-1322356;
 RA Seyffied C.E., Schwelckart V.L., Godiska R., Gray P.W.;
 RT "The human platelet-activating factor receptor gene (PTAFR) contains
 RT no introns and maps to chromosome 1.";
 RL Genomics 13:832-834(1992).
 RN (5)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE-93112021; PubMed-1281995;
 RA Sugimoto T., Tsuchimochi H., McGregor C.G., Mutoh H., Shimizu T.,
 RA Kurachi Y.;
 RT "Molecular cloning and characterization of the platelet-activating
 RT factor receptor gene expressed in the human heart.";
 RL Biochem. Biophys. Res. Commun. 189:617-624(1992).
 RN (6)
 RP SEQUENCE FROM N.A.
 RA Benal R.H., Debussche M.S., Olson M.S.;
 RL Submitted (xxx-1992) to the EMBL/GenBank/DBJ databases.
 RN (7)
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93192035; PubMed-8383507;
 RA Chase P.B., Halonen M., Regan J.W.;
 RT "Cloning of a human platelet-activating factor receptor gene:
 RT evidence for an intron in the 5'-untranslated region.";
 RL Am. J. Respir. Cell Mol. Biol. 8:240-244(1993).
 CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC
 CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
 CC MUSCLE CONTRACTILE AND HYPERTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
 CC ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CC CALCULUM SECOND MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M80436; AAA60001.1; -
 DR EMBL; M76674; AAA60002.1; -
 DR EMBL; D10202; BAA01050.1; -
 DR EMBL; M88177; AAA60214.1; -
 DR EMBL; S52624; AAB24693.2; -
 DR EMBL; L07334; AAA60108.1; -
 DR EMBL; S56396; AAB25755.1; -

DR PIR; JH0479; JH0479.
 DR PIR; A40191; A40191.
 DR PIR; A41079; A41079.
 DR GCRDb; GCR_0186; -
 DR GCRDb; GCR_0260; -
 DR GCRDb; GCR_0285; -
 DR GCRDb; GCR_0414; -
 DR GCRDb; GCR_0478; -
 DR GCRDb; GCR_0548; -
 DR GCRDb; GCR_0731; -
 DR MIM; 173393; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PF01153; PARRECEPTOR.
 DR PROSITE; PS00237; G_PROTEIN_REC_P1.1;
 DR PROSITE; PS0262; G_PROTEIN_REC_P1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis;
 KW Polymorphism.
 FT DOMAIN 1 16
 FT TRANSSEM 17 38
 FT DOMAIN 39 54
 FT TRANSSEM 55 74
 FT DOMAIN 75 91
 FT TRANSSEM 92 113
 FT DOMAIN 114 133
 FT TRANSSEM 134 155
 FT DOMAIN 156 184
 FT TRANSSEM 185 205
 FT DOMAIN 206 233
 FT TRANSSEM 234 254
 FT DOMAIN 255 276
 FT TRANSSEM 277 296
 FT DOMAIN 297 342
 FT DISULFID 90 173
 FT CARBOHYD 169 169
 FT VARIANT 224 224
 FT VARIANT 338 338
 FT VARIANT 338 338
 FT CONFLICT 28 28
 FT CONFLICT 66 66
 FT CONFLICT 95 95
 FT CONFLICT 227 228
 FT CONFLICT 227 228
 FT CONFLICT 247 247
 FT CONFLICT 316 316
 SO SEQUENCE 342 AA; 39203 MW; 89007309EBA79228 CRC64;
 Query Match 22.2%; Score 394; DB 1; Length 342;
 Best Local Similarity 32.6%; Pred. No. 6; 6e-20;
 Matches 107; Conservative 61; Mismatches 134; Indels 26; Gaps 10;
 QY 11 PGNSTICTDYKITYOVLFFPLTYLVLEFVGLITNGLAMRIFFQOR--SKSNFI-IFLKNTY 67
 DB 3 PHDSIMDSEFRYT--LFFIVYSIIIFVLVIAAGVLAWMFARLYPCKKEIKETIFWNL 60
 QY 68 ISDLMLILFFPKILSDAKIGTGLRTFVCOVSVIFEFMYISIFLGIITDRYQKT 127
 DB 61 MADMFLITLPLMITYYQNGMKILPKFLCNVAGCLFFINTYSVAFISYITNRCQAVT 120
 QY 128 RPKFTSNPKNLGAKILSVIVM-----AFMFLSLPNNMILTNROPDRK--NVKCKSEFK 179
 DB 121 RPKITQANTKRKRGISLSLVIVWAIYGAASYFLIDS---TNTVPSAGSGNVTGRC-FEH 176
 QY 180 SEGLVMEHIVANTICOVITMINFLIYIVCYTLTKELKRSYVTRGVGKYPKKRVKVF 239
 DB 177 YKGSVPVLIHIFVIFSEFLVLLIFCNLVITRLMQPVQOORNAEVRRLMW-VC 235
 QY 240 IIAVFICVFPFHAFIRIYTLISOTRDVPCDTAENLTFYKESTLWMTLSINACLDPIYF 299
 DB 236 TVLAVTICFVPHVIVLPTLAEI-LGFDKSRHQAINDAHQVTLCLSLNCAVDLPYIC 294

```

Query Match Similarity 22.1%: Score 392.5: DB 1: Length 342:
Best Local Similarity 30.7%: Pred No. 8,3e-20:
Matches 103, Conservative 66, Mismatches 146, Indels 21, Gaps 9

QY 20 DKRTGVLPFLTYLTFEVLGTLTNGLAMIFPOI--RSKSNFI-IFLKNVTISDLMILT 76
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 10 DSEFRRLTPEPIYSIIIFVLGIITANGVYLWFAFLPYSSKILNEIKIPMVLNLTDLFLT 69
QY 77 FEPKILSDAKLGLGRLTVCQVTSVIFEFPMYIMSSIFGLTIDIXQKTTREPKISNK 136
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 70 LPLMTIYYVSNQGWFLPKFLCNLAGLGFIFINTYCSVAFGLVITYNFQAVKKYPIKTAQAT 129
QY 137 NLGAKILSVLVIV----FEMFLSLPNMILITNRQPRDNKVKCSFLKSEFG----LVNH 187
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 130 TRRGIALSLIVITVAALVAASAFYLWDSITNVYSNKAGSGNITRC-FENHEKSGKPLIITH 188
QY 188 ELVNYTCQYI-FWINEFLIVCYTLLITKELYSYVTRGVGKVPKRKNVKKYFIITAVEF 246
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 189 ----LCIYLGFEFVITLLIFCNLVIITHLLRPVQKQNNAEV-RRRALMNVCTLVAVFV 242
QY 247 ICFVPHFARIPYTLISQTDVDCDAENTLFEYKESTLMLTSLINACLDPIFYFLCKSR 306
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB 243 ICFVPHMQLFWTLAEI-GMPSSNHOQAINDAHQVTLTCLSTNCVLDPVICYFLTKRER 301
QY 307 NSLISMICPNSATSLSDNRKKEODGGDGNBETPM 342
DB 302 KHLSEKLNIMRSSQKSRVTTDTGTETMAIPINHTPV 337

RESULT 8
EBI2_HUMAN
ID EBI2_HUMAN STANDARD: PRT: 361 AA.
AC P32349:
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE EBV-induced G protein-coupled receptor 2 (EBI2).
GN EBI2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93188173; PubMed=8383238;
RA Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,
   Kieff E.;
RT "Epstein-Barr virus-induced genes: first lymphocyte-specific G
RT protein-coupled peptide receptors."
RT J. Virol. 67:2209-2220(1993)
CC -!- FUNCTION: ORPHAN RECEPTOR. PROBABLE MEDIATOR OF EBV EFFECTS ON B
CC LYMPHOCYTES OR OF NORMAL LYMPHOCYTE CELL LINES.
CC -!- TISSUE SPECIFICITY: B-LYMPHOCYTE CELL LINES.
CC -!- INDUCTION: BY EBV.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on CC
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L08177; AAA35924.1; -.
DR PIR: B45680; B45680.
DR GCRdb: GCR_0499; -.
DR MIM: 605741; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.

```

RP SEQUENCE FROM N.A.
RA Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,
RA Ohishi T., Soga T., Matsushime H., Furuichi K.;

[illegible]

```

RESULT 10
PAFR_MOUSE STANDARD; PRT; 341 AA.
ID PAFR_MOUSE
AC 062035;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Platelet activating factor receptor (PAF-R).
GN PAFR.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=96239129; PubMed=8670084;
RA Ishii S., Matsuda Y., Nakamura M., Waga I., Kume K., Izumi T.,
RA Noma M., Shimizu T.;
RT "A murine platelet-activating factor receptor gene: cloning,
RT chromosomal localization and up-regulation of expression by
RT lipopolysaccharide in peritoneal resident macrophages.";
RL Biochem. J. 314:671-678(1996).
CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC
CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
CC ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D50872; BAA09468.1; -.
CC GCRDB: GCR_1618; -.
CC MGD: MGI:106066; Pfaff.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS: PR01153; PAFRECEPTOR.
CC PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; 1.
CC PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Chemotaxis.
CC
CC FT DOMAIN 1 16 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 17 38 1 (POTENTIAL).
CC FT DOMAIN 39 54 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 55 74 2 (POTENTIAL).
CC FT DOMAIN 75 91 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 92 113 3 (POTENTIAL).
CC FT DOMAIN 114 133 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 134 155 4 (POTENTIAL).
CC FT DOMAIN 156 184 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 185 205 5 (POTENTIAL).
CC FT DOMAIN 206 233 CYTOPLASMIC (POTENTIAL).
CC FT TRANSMEM 234 254 6 (POTENTIAL).
CC FT DOMAIN 255 275 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 276 295 7 (POTENTIAL).
CC FT DOMAIN 296 341 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT DISULFID 90 173 BY SIMILARITY.
CC SEQUENCE 341 AA; 39148 MW; CAA8CDDDBD8D26897 CRC64;

```

Query Match

20.68; Score 366; DB 1; Length 341;

```

Best Local Similarity 29.9%; Pred. No. 4.9e-18;
Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;

OY 20 DKITQVLPFLIYTLVFLVGLTNGLAMRIFQI--RSSNFI-IFLKNTVSDLLMIIT 76
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 10 DSEFPTLFPPIVSVIFILGVANGLVFMANLPKSKLINEKIFMVLTMADLLFLIT 69
OY 77 PPFKLSAKLGTGFLRFVCOVTSVIFETVYISISFGLITIDRCKTRPFKTSNPK 136
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 70 LPLMIVYVYNNEDMLPNFLCNVAGCLFFINVCSAFLGVLITNNQAVAPDKRQAT 129
OY 137 NLGAKILSVYIWMF-----FLSLPNMILTNRPDRKNVKKCSFLKSEFG--LWHE 188
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 130 TRKRGISLIIWASIVATASVFLATDSTNLVFNKDGSGNITRCFEPHYEPVILVHY 189
OY 189 IVNYICQVITWTFEL-VIVCTTLITKELYSRVTRGKGVKPKRVNNKVFIIIVFET 247
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 190 FLAFCEFLVFLIFVCNLTIHLLTPMRQO--RRAGV---KRALMMVCTVLAVFTI 243
OY 248 CVPFPHFARIPYTLSTQTRDVCCTAENTLFYVKESTLWLTSLNACDPFIYFLCKSFRN 307
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 244 CVPHHVVOLPPTLAEIG--YQTNFQAIINDAHQITLCLSTNCVDPVITCGLTKKFR 301
OY 308 -----SLISMKCPNSATS 321
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 302 HLEKEFYMSRRSKC-SRATS 321

RESULT 11
PAFR_RAT STANDARD; PRT; 341 AA.
ID PAFR_RAT
AC P46002;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Platelet activating factor receptor (PAF-R).
GN PAFR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=spleen;
RX MEDLINE=94222063; PubMed=8168510;
RA Bito H., Honda Z., Nakamura M., Shimizu T.;
RT "Cloning, expression and tissue distribution of rat
RT platelet-activating-factor-receptor cDNA.";
RL Eur. J. Biochem. 221:211-218(1994).
CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC
CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
CC ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: PRESENT IN ALMOST ALL ORGANS INCLUDING SPLEEN,
CC SMALL INTESTINE, KIDNEY, LUNG, LIVER AND BRAIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U04740; AAA18422.1; -.
CC GCRDB: GCR_0985; -.
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm.1; 1.
CC PRINTS: PR01153; PAFRECEPTOR.
CC PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; 1.

```

DR PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 Chemotaxis.

FT	DOMAIN	1	16	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	17	38	1 (POTENTIAL).
FT	DOMAIN	39	54	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	55	74	2 (POTENTIAL).
FT	DOMAIN	75	91	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	92	113	3 (POTENTIAL).
FT	DOMAIN	114	133	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	134	153	4 (POTENTIAL).
FT	DOMAIN	156	184	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	185	205	5 (POTENTIAL).
FT	DOMAIN	206	233	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	234	254	6 (POTENTIAL).
FT	DOMAIN	255	275	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	276	295	7 (POTENTIAL).
FT	DOMAIN	296	341	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	4	4	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	169	169	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID	90	173	BY SIMILARITY.
SO	SEQUENCE	341 AA:	39204 MW:	DOAEF2290C3D34A5B CRC64;

Query Match 20.4%; Score 362; DB 1; Length 341;
 Best Local Similarity 28.9%; Pred. No. 9.1e-18;
 Matches 96; Conservative 66; Mismatches 120; Indels 50; Gaps 10;

QY 20 DYKTTQVLPFLVTLVLEFVGLITNGLAMRF---FOIRSKSNFIIFLKNTVISDLMLIT 76
 DB 10 DSEFRYTLFPIYVSVIFGLVANGVAVLWVFATLYPSKRLKEIRIFVNLVADLFLFMT 69
 QY 77 FPKRISDAKLTGRLTFRFCOVVSVIFFTMYISIFGLITIDRCKTTRPEKTSMPK 136
 DB 70 LPLMIYVYSEGMIVKFLCNLAGCLFIMTYCSVAFLEITTNRQAVAPYIKTAQAT 129
 QY 137 NLGAKILSVYNAFM-----FLSLPNNMLTNRQPRDKNVKC-----S 176
 DB 130 TRKRGLTSLVIMISIAATASYFLATDSTNVVPRKDSGNTRECEHEPEYSPILVYH 189
 QY 177 ELKSEGLVWHEIVNTCOVIFWNLIVCYTLITKELYSVTRTGKGVKPRKKVNV 236
 DB 190 FITSCFELVEF-----LIFCYNNWII---HTLTPR-----VROQRKEVKKRALMM 233
 QY 237 KVFIIIVFFICVFPFHFARIPYLTROTROVEDCTAENTLFYVKESTWMLSLNACLDPF 296
 DB 234 -VCTVLAVFICFVPHVVOIPMTLAEAG--YQTNFHOAINDAHOITLCLSTNCVDPV 290
 QY 297 IYFELCKSPFN-----SLISMCKCPNSATS 321
 DB 291 IYCFELTKFKRKHLESEKFSMRSSKRC-SRATS 321

RESULT 12
 P2Y5_CHICK STANDARD: PRT: 308 AA.
 ID P2Y5_CHICK
 AC P32250;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE P2Y purinoceptor 5 (P2Y5) (Purinergic receptor 5) (6nl).
 GN P2RY5.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RX NCBI_TaxID=9031;
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RA MEDLINE=93329058; PubMed=8393036;
 RA Kaplan M.H., Smith D.I., Sundick R.S.;
 RT Identification of a G protein coupled receptor induced in activated

RT T cells.";
 RL J. Immunol. 151:628-636(1993).
 CC - SUBCELLULAR LOCATION: Integral membrane protein.
 CC - TISSUE SPECIFICITY: INDUCED IN ACTIVATED T-CELLS.
 CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: L06109; AAB06387.1; -
 DR HSSP: P34996; IDDD.
 DR GCRDB; GCR_0689; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7cm1.1.
 DR PRINTS: PR01157; P2Y5PRNOCEPR.
 DR PRINTS: PR01157; P2Y5PRNOCEPR.
 DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
 DR PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Lipoprotein;
 KW Palmitate.

FT	DOMAIN	1	16	EXTRACELLULAR (POTENTIAL).
FT <th>DOMAIN</th> <td>17</td> <td>43</td> <td>1 (POTENTIAL).</td>	DOMAIN	17	43	1 (POTENTIAL).
FT <th>DOMAIN</th> <td>44</td> <td>52</td> <td>CYTOPLASMIC (POTENTIAL).</td>	DOMAIN	44	52	CYTOPLASMIC (POTENTIAL).
FT <th>DOMAIN</th> <td>53</td> <td>76</td> <td>2 (POTENTIAL).</td>	DOMAIN	53	76	2 (POTENTIAL).
FT <th>DOMAIN</th> <td>77</td> <td>89</td> <td>EXTRACELLULAR (POTENTIAL).</td>	DOMAIN	77	89	EXTRACELLULAR (POTENTIAL).
FT <th>DOMAIN</th> <td>90</td> <td>109</td> <td>3 (POTENTIAL).</td>	DOMAIN	90	109	3 (POTENTIAL).
FT <th>DOMAIN</th> <td>110</td> <td>130</td> <td>CYTOPLASMIC (POTENTIAL).</td>	DOMAIN	110	130	CYTOPLASMIC (POTENTIAL).
FT <th>DOMAIN</th> <td>131</td> <td>151</td> <td>4 (POTENTIAL).</td>	DOMAIN	131	151	4 (POTENTIAL).
FT <th>DOMAIN</th> <td>152</td> <td>178</td> <td>EXTRACELLULAR (POTENTIAL).</td>	DOMAIN	152	178	EXTRACELLULAR (POTENTIAL).
FT <th>DOMAIN</th> <td>179</td> <td>206</td> <td>5 (POTENTIAL).</td>	DOMAIN	179	206	5 (POTENTIAL).
FT <th>DOMAIN</th> <td>207</td> <td>224</td> <td>CYTOPLASMIC (POTENTIAL).</td>	DOMAIN	207	224	CYTOPLASMIC (POTENTIAL).
FT <th>DOMAIN</th> <td>225</td> <td>250</td> <td>6 (POTENTIAL).</td>	DOMAIN	225	250	6 (POTENTIAL).
FT <th>DOMAIN</th> <td>251</td> <td>269</td> <td>EXTRACELLULAR (POTENTIAL).</td>	DOMAIN	251	269	EXTRACELLULAR (POTENTIAL).
FT <th>DOMAIN</th> <td>270</td> <td>289</td> <td>7 (POTENTIAL).</td>	DOMAIN	270	289	7 (POTENTIAL).
FT <th>DOMAIN</th> <td>290</td> <td>308</td> <td>CYTOPLASMIC (POTENTIAL).</td>	DOMAIN	290	308	CYTOPLASMIC (POTENTIAL).
FT <th>CARBOHYD</th> <td>5</td> <td>5</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td>	CARBOHYD	5	5	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <th>CARBOHYD</th> <td>281</td> <td>281</td> <td>PALMITATE (BY SIMILARITY).</td>	CARBOHYD	281	281	PALMITATE (BY SIMILARITY).
FT <th>DISULFID</th> <td>86</td> <td>165</td> <td>POTENTIAL.</td>	DISULFID	86	165	POTENTIAL.
SO	SEQUENCE	308 AA:	35597 MW:	4214E96933B6F7D CRC64;

Query Match 20.1%; Score 357.5; DB 1; Length 308;
 Best Local Similarity 29.5%; Pred. No. 1.7e-17;
 Matches 87; Conservative 68; Mismatches 125; Indels 15; Gaps 8;

QY 14 TSLCTRDYKITOVLPFLVTLVLEFVGLITNGLAMRF-FOIRSKSNFIIFLKNTVISDL 72
 DB 3 SSGSTEDSEFKYTLVGCVEFMVFLGLIANCAVIFFTLKRNNETTYMLMAISDL 62
 QY 73 MLTPEPKILSDAKLTGRLTFRFCOVVSVIFFTMYISIFGLITIDRCKTTRPEKT 132
 DB 63 EYFTLPFRKIYFV-VANMPFGVLYCKISVLTFTNMGSLFTLCISVDPLAIYHPFRS 121
 QY 133 SNPKNLGAKILSVYNAFMFLSLPNNMLT--TNROPDRKNVKK--SFLKSEGLWHE 188
 DB 122 KILTRKRNARIVCAVAVITVLAGSTPASFQSTNRQ--NNTQKTCENPFESHWKTYLSR 180
 QY 189 IYNYICOVIFWNLIVCYTLITKELYSVTRTGKGVKPRKKVNVKVFIIIAVFIC 248
 DB 181 IYFIEIVGFPIPLINVTGSTMVLTLPKPLTLRS--NLSKKKVKLMIFVHLVLCFC 238
 QY 249 FVPEHFRIPYLTROTROVEDCTAENTLFYVKESTWMLSLNACLDPEIIEF 300
 DB 239 FVYNTITLILSLMRQTWINGSVYAVRIMPV---TLCIAVSNCCDFPIYVF 290

RESULT 13
 CLT2_HUMAN

ID CLT2 HUMAN STANDARD; PRT; 346 AA.
AC Q9NS75; Q9HCO2; 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last sequence update)
DR Cysteinyln leukotriene receptor 2 (CysLTR2) (P5ECO146) (HG57) (HPN321).
GN CysLTR2 OR CysLTR2 OR CysLTR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20374466; PubMed=10913337;
RA Takasaki J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Ota T.,
RA Nishikawa T., Kawal Y., Masuno Y., Isogai T., Suzuki Y., Sugano S.,
RA Furuichi K.;
RT "The molecular characterization and tissue distribution of the human
RT cysteinyl leukotriene CysLTR2 receptor";
RL Biochem. Biophys. Res. Commun. 274:316-322(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20459128; PubMed=10851239;
RA Heise C.E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T.,
RA Im D.-S., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R.,
RA Williams D.L., Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N.,
RA Liu Y., Austin C.P., George S.R., O'Neill G.P., Metters K.M.,
RA Lynch K.R., Evans J.F.;
RT "Characterization of the human cysteinyl leukotriene 2 receptor";
RL J. Biol. Chem. 275:30531-30536(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX PubMed=11093801;
RA Notack H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,
RA Civelli O.;
RT "Molecular cloning and characterization of a second human cysteinyl
RT leukotriene receptor: discovery of a subtype selective agonist";
RL Mol. Pharmacol. 58:1601-1608(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Dunn M.;
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 17-346 FROM N.A.
RA Suga H.;
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
CC mediated via a G-protein that activates a phosphatidylinositol-
CC calcium second messenger system. Stimulation by BAY u9773, a
CC partial agonist, induces specific contractions of pulmonary veins
CC and might also have an indirect role in the relaxation of the
CC pulmonary vascular endothelium. The rank order of affinities for
CC the leukotrienes is LTC4 > LTD4 > LTE4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed, with highest levels in the
CC heart, placenta, spleen, peripheral blood leukocytes and adrenal
CC gland. In lung, expressed in the interstitial macrophages, and
CC slightly in smooth muscle cells.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB038269; BAB03601.1; -
DR EMBL: AF254664; AAC17281.1; -
DR EMBL: AF279611; AAK69485.1; -

DR EMBL: AL137118; CAC29102.1; -
DR EMBL: AB041644; BAB16379.1; -
DR MIM: 605666; -
DR InterPro: IPR004071; CysLeuk_receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR01533; CysLTR2CPTR.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00262; G_PROTEIN_REC_F1_2; 1. FALSE_NEG.
DR PROSITE: PS00262; G_PROTEIN_REC_F1_2; 1. FALSE_NEG.
KW G-protein coupled receptor; Transmembrane; glycoprotein.
FT DOMAIN 1 42
FT TRANSMEM 43 63
FT DOMAIN 64 72
FT TRANSMEM 73 93
FT DOMAIN 94 123
FT TRANSMEM 124 144
FT DOMAIN 145 153
FT TRANSMEM 154 174
FT TRANSMEM 175 204
FT TRANSMEM 205 225
FT TRANSMEM 226 245
FT TRANSMEM 246 266
FT DOMAIN 267 286
FT TRANSMEM 287 307
FT DOMAIN 308 346
FT DISULFID 111 187
FT CAROXYD 20 26
FT CAROXYD 30 36
FT CAROXYD 181 181
FT CAROXYD 181 181
SQ SEQUENCE 346 AA; 39635 MW; EBS4A4A2DDCESEEA CRC64;

Query Match 19.5%; Score 347.5; DB 1; Length 346;
Best Local Similarity 29.0%; Pred. No. 8.6e-17;
Matches 93; Conservative 68; Mismatches 129; Indels 31; Gaps 10;

QY 6 NLTSAGNNTSLCTRDYKIQVFLPLLYTLFEGTLTNGIAMIPIQIRKSNFI-IFLK 64
DB 20 NGTFSSNNRNRCITIE-NFRREFPIYVLIIFMGVANGSIYVFPQYKKSIVNVEML 78
QY 65 NTVISDLMITLTPPK-----ILSDAKIGTGPPLRTFVCOVTVSYFFYFMYISIF 114
DB 79 NLAISDLFIISLPFRADYLYRGSNMIFGD-----LACRIMSYSLYVMYSIYF 128
QY 115 LGITTDYRQKTRTPKTSNPKMLGAKILISVYMAFMFLSPNMLTRORPKRWK 174
DB 129 LTVLSVGRFLVAVHPRLVHSIRSAMWILGITMLIMASSI--MLDSGSEQNGSVTS 186
QY 175 GSFLKSEFLVWHEIVNYICOVI-EWINFLIVCYTLITKELYSRVYRTGVGKYPKK 233
DB 187 CLEL-NLYKIAKQIPNNYIALVGCGLPPFTLSICVLLIRVLLKVEVPSG-RVSHRK 244
QY 234 VNVKVFITIAVFICVPPHFAPIPTLSOTRVPFCTAENTLFYKESITLMLTSLNACL 293
DB 245 ALTTITITLITLIFLCPLPHLTPTVHL--TTWVGILC-KDRLLKALVITLALANACF 300
QY 294 DPFIYFLCKSPFNLSIMUK 314
DB 301 NPLIYFAGEHFKDRKLSALR 321
RESULT 14
P2Y8_XENLA
ID P2Y8_XENLA STANDARD; PRT; 537 AA.
AC P79928;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE P2Y purinoceptor 8 (P2Y8).
GN Xenopus laevis (African clawed frog).

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2002, 15:30:22 ; Search time 28.74 Seconds
(without alignments)
2058.604 Million cell updates/sec

Title: US-09-827-937A-2

Perfect score: 1778

Sequence: 1 MQAVDNLTSAPGNTSLCTR.....SODNRKKEDGDGDPNETPM 342

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_19:*
2: SP_archaea:*
3: SP_bacteria:*
4: SP_fungi:*
5: SP_human:*
6: SP_invertebrate:*
7: SP_mammal:*
8: SP_mhc:*
9: SP_organelle:*
10: SP_phage:*
11: SP_plant:*
12: SP_rodent:*
13: SP_virus:*
14: SP_vertibrate:*
15: SP_unclassified:*
16: SP_rvirts:*
17: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1778	100.0	342	4	Q9H244	Q9H244 homo sapien
2	1748	98.3	342	6	Q9BGT8	Q9BGT8 macaca fasc
3	1748	98.3	342	6	Q9SKC3	Q9SKC3 macaca fasc
4	1555.5	87.5	347	11	Q9CPV9	Q9CPV9 mus musculu
5	1528.5	86.0	343	11	Q9EPX4	Q9EPX4 rattus norv
6	829	46.6	333	4	Q9BPV8	Q9BPV8 homo sapien
7	794	44.7	337	11	Q9DBI2	Q9DBI2 mus musculu
8	741.5	41.7	338	11	Q9ESG6	Q9ESG6 mus musculu
9	699.5	39.3	358	4	Q9GJZ8	Q9GJZ8 mus sapien
10	694.5	39.1	358	4	Q9BY21	Q9BY21 homo sapien
11	685.5	38.6	359	11	Q9BWT7	Q9BWT7 mus musculu
12	559	31.4	228	6	Q9BE53	Q9BE53 macaca fasc
13	553.5	31.1	229	4	Q9BYC2	Q9BYC2 homo sapien
14	448	25.2	176	4	Q9BVI1	Q9BVI1 homo sapien
15	388.5	21.9	342	6	Q9TIV5	Q9TIV5 bos taurus
16	387.5	21.8	342	6	Q9GK76	Q9GK76 capra hircu

17	368.5	20.7	296	6	Q9TYV6	Q9TYV6 canis fami
18	367	20.6	345	6	Q95N03	Q95N03 sus scrofa
19	365	20.5	342	6	Q9XSD4	Q9XSD4 sus scrofa
20	356	20.0	374	13	Q57466	Q57466 melagris g
21	347.5	19.5	330	4	Q9HCQ2	Q9HCQ2 homo sapien
22	347.5	19.5	346	4	Q9NS75	Q9NS75 homo sapien
23	344	19.3	309	11	Q920A1	Q920A1 mus musculu
24	343	19.3	359	13	Q9PVY7	Q9PVY7 anguilla an
25	339.5	19.1	309	11	Q924T9	Q924T9 rattus norv
26	338	19.0	359	6	Q9N0U1	Q9N0U1 ovis aries
27	334	18.8	367	4	Q9UE21	Q9UE21 homo sapien
28	328	18.4	340	6	Q95N02	Q95N02 sus scrofa
29	322	18.1	359	11	Q9EPD3	Q9EPD3 cavia porce
30	321	18.1	359	6	Q9GLN9	Q9GLN9 pan troglod
31	318	17.9	361	11	Q9JIS7	Q9JIS7 mus musculu
32	316	17.8	377	11	Q9JHG3	Q9JHG3 rattus norv
33	314	17.7	400	6	Q95M54	Q95M54 macaca fasc
34	311	17.5	361	11	Q95811	Q95811 rattus norv
35	309.5	17.4	298	4	Q9UDZ6	Q9UDZ6 homo sapien
36	309.5	17.4	339	11	Q924T8	Q924T8 rattus norv
37	309	17.4	358	13	Q9PUA0	Q9PUA0 acipenser r
38	309	17.4	454	4	Q9H573	Q9H573 homo sapien
39	308	17.3	400	6	Q9MTW9	Q9MTW9 macaca mula
40	307	17.3	359	11	Q9EOR9	Q9EOR9 meriones un
41	304.5	17.1	339	11	Q9J7J1	Q9J7J1 mus musculu
42	304.5	17.1	352	11	Q99J44	Q99J44 mus musculu
43	304.5	17.1	393	11	Q9R1M0	Q9R1M0 mus musculu
44	304.5	17.1	401	11	Q9R1I9	Q9R1I9 mus musculu
45	304.5	17.1	438	11	Q9R0D1	Q9R0D1 mus musculu

ALIGNMENTS

Q9H244	PRELIMINARY:	PRT:	342 AA.
AC Q9H244:			
DT 01-MAR-2001 (TREMBLrel. 16, Created)			
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE P2Y12 PLATELET ADP RECEPTOR (G-PROTEIN COUPLED RECEPTOR SP1999)			
DE (GI-CPDLEAD ADP RECEPTOR HOKK3).			
GN HOKK3.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=21037966; PubMed=11196645;			
RA Hollinger G., Jantzen H.-M., Vincent D., Li G., England L.,			
RA Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J.,			
RA Conley P.B.;			
RT "Identification of the Platelet ADP Receptor Targeted by			
RT Antithrombotic Drugs.;"			
RL Nature 409:202-207(2001).			
RN [2]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=21269433; PubMed=11104774;			
RA Zhang F.L., Luo L., Gustafson E., Lachowicz J., Smith M., Qiao X.,			
RA Liu Y.-H., Chen G., Pramanik B., Laz T.M., Palmer K., Bayne M.,			
RA Momena F.J. Jr.;			
RT "ADP is the cognate ligand for the orphan G protein-coupled receptor			
RT SP1999.;"			
RL J. Biol. Chem. 276:8608-8615(2001).			
RN [3]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=21394281; PubMed=11502873;			
RA Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.,			
RA Ohishi T., Soga T., Matsushima H., Furuichi K.;			
RT "Molecular cloning of the platelet P2YAC ADP receptor.;"			
RT Pharmacological comparison with another ADP receptor, the P2Y1			

RT receptor.";
 RL Mol. Pharmacol. 60:432-439(2001).
 DR EMBL: AF313449; AAC48944.1; -;
 DR EMBL: AF321815; AAK00948.1; -;
 DR EMBL: AB052684; BAB60824.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPS.
 DR PROSITE: PS50262; G_PROTEIN_RECER_FL_2; 1.
 KW Receptor.
 SQ SEQUENCE 342 AA; 39438 MW; 8553D2746C89176D CRC64;

Query Match 100.0%; Score 1778; DB 4; Length 342;
 Best Local Similarity 100.0%; Pred. No. 3.4e-151;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOAVDNLTSAPGNTSLCTRDYKITQVLEFLLYVLEFVGLITNGLAMRIFFOIRKSNFI 60
 DB 1 MOAVDNLTSAPGNTSLCTRDYKITQVLEFLLYVLEFVGLITNGLAMRIFFOIRKSNFI 60
 QY 61 IFLKNTVISDLMLITLPPFKILSDAKLGTGRLTFVCQVSVIFETMYISISFLGLITI 120
 DB 61 IFLKNTVISDLMLITLPPFKILSDAKLGTGRLTFVCQVSVIFETMYISISFLGLITI 120
 QY 121 DRYQKTRPFTSNPKNLGAKILSVIVIAFMFLSLPNMILTNRPDRDNVKKCSFLKS 180
 DB 121 DRYQKTRPFTSNPKNLGAKILSVIVIAFMFLSLPNMILTNRPDRDNVKKCSFLKS 180
 QY 181 EFGLVWHEIVNYICQVIFWNLIVICVYTLITKELRSYVTRGVGKVRKKNVAVFI 240
 DB 181 EFGLVWHEIVNYICQVIFWNLIVICVYTLITKELRSYVTRGVGKVRKKNVAVFI 240
 QY 241 IIAVFICVPPHFARIPYTLISQTRDVPDCTAENTLFFYKESTLMTLSNACLDPEIFYE 300
 DB 241 IIAVFICVPPHFARIPYTLISQTRDVPDCTAENTLFFYKESTLMTLSNACLDPEIFYE 300
 QY 301 LCKSFNLSLSMLKCPNSATSLSDNRKKEODGDPNEETPM 342
 DB 301 LCKSFNLSLSMLKCPNSATSLSDNRKKEODGDPNEETPM 342

RESULT 2
 Q9BGT8 PRELIMINARY; PRT; 342 AA.
 ID Q9BGT8;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE HYPOTHETICAL 39.5 KDA PROTEIN.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=FRONTAL LOBE LEFT;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RA "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB056385; BAB33041.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHHODOPS.
 DR PROSITE: PS50262; G_PROTEIN_RECER_FL_2; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 342 AA; 39497 MW; 3D21BF987FC48599 CRC64;

Query Match 98.3%; Score 1748; DB 6; Length 342;

Best Local Similarity 98.0%; Pred. No. 1.6e-148;
 Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MOAVDNLTSAPGNTSLCTRDYKITQVLEFLLYVLEFVGLITNGLAMRIFFOIRKSNFI 60
 DB 1 MOAVDNLTSAPGNTSLCTRDYKITQVLEFLLYVLEFVGLITNGLAMRIFFOIRKSNFI 60
 QY 61 IFLKNTVISDLMLITLPPFKILSDAKLGTGRLTFVCQVSVIFETMYISISFLGLITI 120
 DB 61 IFLKNTVISDLMLITLPPFKILSDAKLGTGRLTFVCQVSVIFETMYISISFLGLITI 120
 QY 121 DRYQKTRPFTSNPKNLGAKILSVIVIAFMFLSLPNMILTNRPDRDNVKKCSFLKS 180
 DB 121 DRYQKTRPFTSNPKNLGAKILSVIVIAFMFLSLPNMILTNRPDRDNVKKCSFLKS 180
 QY 181 EFGLVWHEIVNYICQVIFWNLIVICVYTLITKELRSYVTRGVGKVRKKNVAVFI 240
 DB 181 EFGLVWHEIVNYICQVIFWNLIVICVYTLITKELRSYVTRGVGKVRKKNVAVFI 240
 QY 241 IIAVFICVPPHFARIPYTLISQTRDVPDCTAENTLFFYKESTLMTLSNACLDPEIFYE 300
 DB 241 IIAVFICVPPHFARIPYTLISQTRDVPDCTAENTLFFYKESTLMTLSNACLDPEIFYE 300
 QY 301 LCKSFNLSLSMLKCPNSATSLSDNRKKEODGDPNEETPM 342
 DB 301 LCKSFNLSLSMLKCPNSATSLSDNRKKEODGDPNEETPM 342

RESULT 3
 Q95KC3 PRELIMINARY; PRT; 342 AA.
 ID Q95KC3;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE HYPOTHETICAL 39.5 KDA PROTEIN.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MEDULLA OBLONGATA;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RA "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB062981; BAB60747.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 342 AA; 39479 MW; E93FC26BFF5EC4C CRC64;

Query Match 98.3%; Score 1748; DB 6; Length 342;
 Best Local Similarity 98.0%; Pred. No. 1.6e-148;
 Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MOAVDNLTSAPGNTSLCTRDYKITQVLEFLLYVLEFVGLITNGLAMRIFFOIRKSNFI 60
 DB 1 MOAVDNLTSAPGNTSLCTRDYKITQVLEFLLYVLEFVGLITNGLAMRIFFOIRKSNFI 60
 QY 61 IFLKNTVISDLMLITLPPFKILSDAKLGTGRLTFVCQVSVIFETMYISISFLGLITI 120
 DB 61 IFLKNTVISDLMLITLPPFKILSDAKLGTGRLTFVCQVSVIFETMYISISFLGLITI 120
 QY 121 DRYQKTRPFTSNPKNLGAKILSVIVIAFMFLSLPNMILTNRPDRDNVKKCSFLKS 180
 DB 121 DRYQKTRPFTSNPKNLGAKILSVIVIAFMFLSLPNMILTNRPDRDNVKKCSFLKS 180
 QY 181 EFGLVWHEIVNYICQVIFWNLIVICVYTLITKELRSYVTRGVGKVRKKNVAVFI 240
 DB 181 EFGLVWHEIVNYICQVIFWNLIVICVYTLITKELRSYVTRGVGKVRKKNVAVFI 240

OY 241 IIAVFICFVPHFARIPYTLSDRDVDCDAENTLFFVKESTLMTLSLNACLDPEFIYF 300
DB 241 IIAVFICFVPHFARIPYTLSDRDVDCDAENTLFFVKESTLMTLSLNACLDPEFIYF 300
OY 301 LCKSFNLSLMLKCPNSATSLSODNRKKKQDGDGPNEETPM 342
DB 301 LCKSFNLSLMLKCPNSATSLSODNRKKKQDGDGPNEETPM 342

RESULT 4

OY 09CPV9 PRELIMINARY: PRT: 347 AA.
AC 09CPV9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 4921504D23RIK PROTEIN (2900079B22RIK PROTEIN).
GN P2RY12 OR 4921504D23RIK OR 2900079B22RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS, AND HIPPOCAMPUS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Aizawa K., Izawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
R Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
Kuehl P., Lewis S., Matsuo Y., Nishida I., Pesole G., Quackenbush J.,
Schlitz L.M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Oikido T., Furuno M., Aono H., Balderelli R., Barsh G.,
Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
Hayashizaki Y.;
RT *Functional annotation of a full-length mouse cDNA collection.*;
RL Nature 409:685-690(2001).
DR EMBL: AK014807; BAB29561.1; -;
DR EMBL: AK014804; BAB29000.1; -;
DR MGD: MGI:1918089; P2RY12.
DR MGD: MGI:1920308; 2900079B22RIK.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS50262; G_PROTEIN_RECIP_F1_2; 1.
SQ SEQUENCE 347 AA; 39473 MW; F107488E57E025F1 CRC64;

Query Match 87.5%; Score 1555.5; DB 11; Length 347;
Best Local Similarity 88.7%; Pred. No. 2,7e-131;
Matches 299; Conservative 16; Mismatches 21; Indels 1; Gaps 1;
OY 6 NLTSAPGNTSLCTRDYKKTQVLEPLLYTVLFFVGLITNGLAMRIFQIRKSNFIIFLKN 65
DB 12 NTFISGCTSLCVRDKITQVLEPLLYTVLFFVGLITNSLAMRIFQIRKSNFIIFLKN 71
OY 66 TVISDLMLITLFFPKILSDAKLGTPLRTFVCOVTSVIFFTMYISISFLGLITIDRYOK 125
DB 72 TVISDLMLITLFFPKILSDAKLGTPLRTFVCOVTSVIFFTMYISISFLGLITIDRYOK 131
OY 126 TTRPFTSNPKNLGAKILSVIYAWMFLSLPNNMILTNROPDKNVKCSFLKSEGLV 185
DB 132 TTRPFTSNPKNLGAKILSVIYAWMFLSLPNNMILTNRRPKDKVTKCSFLKSEGLV 191

OY 186 WHEIYNYICQVIFWNTLIVICYTLITKELYRSYVTRGVGVKPKKVVKKVFIIAVF 245
DB 192 WHEIYNYICQVIFWNTLIVICYSLITKELYRSYVTRGSAVKKVKKVFIIAVF 251
OY 246 FICFVPHFARIPYTLSDRDVDCDAENTLFFVKESTLMTLSLNACLDPEFIYFICKSF 305
DB 252 FICFVPHFARIPYTLSDRDVDCDAENTLFFVKESTLMTLSLNACLDPEFIYFICKSF 311
OY 306 RNSLSMLKCPNSATSLSODNRKKKQDGDGPNEETPM 342
DB 312 RNSLSMLKCPNSATSLSODNRKKKQDGDGPNEETPM 347

RESULT 5

OY 09EPX4 PRELIMINARY: PRT: 343 AA.
AC 09EPX4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE P2Y12 PLATELET ADP RECEPTOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=21037966; PubMed=1196645;
RA Hollreiter G., Jantzen H.-M., Vincent D., Li G., England L.,
Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J.,
Conley P.B.;
RT "Identification of the Platelet ADP Receptor Targeted by
Antithrombotic Drugs";
RL Nature 409:202-207(2001).
DR EMBL: AF134450; AAC48945.1; -;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS50262; G_PROTEIN_RECIP_F1_2; 1.
DR KW Receptor.
SQ SEQUENCE 343 AA; 39047 MW; 7AE0ARCE66674136 CRC64;

Query Match 86.0%; Score 1528.5; DB 11; Length 343;
Best Local Similarity 86.9%; Pred. No. 6,9e-129;
Matches 293; Conservative 17; Mismatches 22; Indels 5; Gaps 1;

OY 6 NLTSAPGNTSLCTRDYKKTQVLEPLLYTVLFFVGLITNGLAMRIFQIRKSNFIIFLKN 65
DB 12 NTFISGCTSLCVRDKITQVLEPLLYTVLFFVGLITNSLAMRIFQIRKSNFIIFLKN 71
OY 66 TVISDLMLITLFFPKILSDAKLGTPLRTFVCOVTSVIFFTMYISISFLGLITIDRYOK 125
DB 72 TVISDLMLITLFFPKILSDAKLGTPLRTFVCOVTSVIFFTMYISISFLGLITIDRYOK 131
OY 126 TTRPFTSNPKNLGAKILSVIYAWMFLSLPNNMILTNROPDKNVKCSFLKSEGLV 185
DB 132 TTRPFTSNPKNLGAKILSVIYAWMFLSLPNNMILTNRRPKDKVTKCSFLKSEGLV 191
OY 186 WHEIYNYICQVIFWNTLIVICYTLITKELYRSYVTRGVGVKPKKVVKKVFIIAVF 245
DB 192 WHEIYNYICQVIFWNTLIVICYSLITKELYRSYVTRGSAVKKVKKVFIIAVF 251
OY 246 FICFVPHFARIPYTLSDRDVDCDAENTLFFVKESTLMTLSLNACLDPEFIYFICKSF 305
DB 252 FICFVPHFARIPYTLSDRDVDCDAENTLFFVKESTLMTLSLNACLDPEFIYFICKSF 311
OY 306 RNSLSMLKCPNSATSLSODNRKKKQDGDGPNEETPM 342
DB 312 RNSLSMLKCPNSATSLSODNRKKKQDGDGPNEETPM 343

```

RESULT 6
Q9BPV8 PRELIMINARY; PRT; 333 AA.
AC Q9BPV8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE G-PROTEIN-COUPLED RECEPTOR FKS677 (G-PROTEIN COUPLED RECEPTOR GPR86) (G PROTEIN-COUPLED RECEPTOR)
DE GPR86)
GN FKS677 OR GPR86 OR GPR94.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA Wang Y., Gong L.;
RT "Molecular cloning of FKS677, a novel gene encoding a putative G-protein-coupled receptor."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21172992; PubMed=11273702;
RT "An expressed sequence tag (est) data mining strategy succeeding in the discovery of new G-protein coupled receptors."
RL J. Mol. Biol. 307:799-813(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21458557; PubMed=11574155;
RT Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantli W.B., Arkhitko O., Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor genes."
RL Gene 275:83-91(2001).
RN [4]
RP SEQUENCE FROM N.A.
RX PubMed=11546776;
RA Communi D., Gonzalez N.S., Dethieux M., Brezillon S., Lannoy V., Parmentier M., Boeynaems J.M.;
RT "Identification of a Novel Human ADP Receptor Coupled to G1."
RL J. Biol. Chem. 276:4179-4185(2001).
DR EMBL: AF345565; AAK29068.1; -
DR EMBL: AF295368; AAK01864.1; -
DR EMBL: AF411113; AAL26484.1; -
DR EMBL: AF40692; AAL01038.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G-PROTEIN_REC_P1_1; UNKNOWN_1.
DR PROSITE: PS50262; G-PROTEIN_REC_P1_2; 1.
KW RECEPTOR.
SQ 333 AA; 38440 MW; F234AB50016DF34 CRC64;

```

Query Match 46.6%; Score 829; DB 4; Length 333;
 Best Local Similarity 49.1%; Pred. No. 2.4e-66;
 Matches 153; Conservative 57; Mismatches 102; Indels 2; Gaps 1;

```

QY 17 CTFDYKTYQVLPFLYVLFVGLITNGLAMRIFFOIRSKSNFIILKNTVISDLMLIT 76
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 15 CPDRTYQVLPFLYVLFVGLITNGLAMRIFFOIRSKSNFIILKNTVISDLMLIT 74
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 77 EPRKISDAKLGTPRTVCQVTSVIFFTMYISISFLGILITDRYQKTRPEKTSMPK 136
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 75 LPRKISDSHLAPWQLRAFCRFSSVIFETMYGIVLGLIAEDRFLKIIRPLRNIFLK 134
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 137 NLGAKLISVIVNAFMELLSPNNILTNROKDNVKKCSLKSSEGLVWHEIVYICOV 196
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 135 KPVFAKTVSIFWFLPFLISLPNMLISNKEATPSSVKKCASLGKPLKHMOWNNICOF 194
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

QY 197 IEMINELIIVCYTLITKEIYSYVTRGVGKVPKRKVNVKVFIIIAVFCIFVPEHAR 256
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 195 IFWYFIIIMLVFYVIAKAYDSIRKSKKRNKKLEGKPFVVAVFVFCAPPHFAR 254
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 257 IPYTLISQTRVDFDCTAENTLTFYKESTIMLTLNACLDPEIFYFLCKSFRLNISLAKCP 316
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 255 VPTYSQNNKNDKDCQLQNOFLFAKETTLFLAATNICMDPLIYIFLCKFTEKLPQWQ--G 312
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 317 NSATLSQDNKKKED 332
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 313 RKTPTASQENHSSQPD 328
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

Query Match 44.7%; Score 794; DB 11; Length 337;
 Best Local Similarity 45.9%; Pred. No. 3.2e-63;
 Matches 151; Conservative 63; Mismatches 111; Indels 4; Gaps 3;

```

QY 6 NLTSPAG--NTSLCTRDYKITQVLPFLYVLFVGLITNGLAMRIFFOIRSKSNFIIFL 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 NTGQGFENKSERCPDRTMTQLPFLYVLFVGLITNGLAMRIFFOIRSKSNFIIFL 65
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 KNTVISDLMLITLTPFKIISDAKLGTPRTVCQVTSVIFFTMYISISFLGILITDRY 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 KNTIVADLIMLALMPKRIISDSHLAPWQLRGFCITLSSVVFETMYVGIMMGLIAEDFR 125
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

[illegible]

RESULT	ID	QSESG6	PRELIMINARY:	PRT:	338 AA.
AC	QSESG6				
DT	01-MAR-2001	(TREMBLrel, 16, Created)			
DT	01-MAR-2001	(TREMBLrel, 16, Last sequence update)			
DT	01-JUN-2001	(TREMBLrel, 17, Last annotation update)			
DE	7 TRANSMEMBRANE G-PROTEIN COUPLED RECEPTOR.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus				
OX	NCBI_TaxId=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Lee B.C., Scadden D.T.;				
RT	"7 transmembrane G protein coupled receptor from hematopoietic				
RT	progenitors.";				
RL	Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL, AF177211, AAC09275.1;				
DR	InterPro: IPR000276; GPCR_Rhodopsn.				
DR	Pfam: PF00001; 7tm_1, 1.				
DR	PRINTS: PR00237; GPCRHDOPSN.				
DR	ProSITE: PS50262; G_PROTEIN_RECPT_FL_2, 1.				
KW	Receptor; Transmembrane.				
SO	SEQUENCE				
	338 AA;				
	38661 MW;				
	43765062226684AE CRC64;				

Query Match	41.78;	Score 741.5;	DB 11;	Length 338;	..
Best Local Similarity	44.18;	Pred. No. 1.6e-58;			..
Matches 146; Conservative	69;	Mismatches 109;	Indels 7;	Gaps 3	

Qy	4	VDNLTSSAGNLSCTBRYKIQVQFPLLYIVLFEVGTGTLGMLRIEFOJRSKSNFIIFL	63
Db	1	MNNSFTTDDPNOQCSMWTLITKQIILPVLYGWFVITGILLNGISGMWIFFYPPSSKSFITVL	60
Qy	64	KNYVYSIDLMLITPPFKILSDAKIGTGPRLTFCVQVTSVIFFTYMWISISFLCLITIDRY	1233
Db	61	KNIVYAFGLMGTPEFVPLDGSGLPQVNVAFVCRSAVTEFYVNMVYSIVFELISIDRY	1200
Qy	124	QKTRPEKTSNPKNMLLAKILSVYIAFMFELSLPNMILINROPDRKCNVYKCSFLKSEFG	1833
Db	121	YKIKPLLTSTVQSVNYSKLLSLVYMWMLMLLLAVPNILINQGVKEVTKIQCHELNELG	1800
Qy	184	LVHMEIYVIGQVTFWJNFILVICYTLITKELRYSVTRGVGRKKNVKNVFIITIA	2433
Db	181	RKMHKASNYIYVSIFFWVFLLLIYFYATIRKIFKSHLKRKKNSTSVYKRKSSNIFISIVL	2400
Qy	244	VFFICFVNFHRIAPYTLISQTRDVFCDCTAETLTFYVHSESTLMTLSLACDPRITFELCK	3033
Db	241	VFVVCVPFYHRIARIPYKTSQDEGHSICRTMETLLYAKNEFTLLLSAANVCDDPIITIFFLCO	3000
Qy	304	SFR---NSLSIM-LKCRSATSLSDONRKKE	330
Db	301	PFREVLNKKLHMSLKVN---DEVSVKTKRE	328

RESULT	9
096J28	
ID	096J28
AC	096J28;
DT	01-DEC-2001 (Tremblrel. 19, Created)
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE	CDNA FL114878 FIS. CLONE PLACE1003238, WEAKLY SIMILAR TO PROBABLE
DE	G PROTEIN-COUPLED RECEPTOR.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX	NCBI_TaxID=9606;
	[1]
RP	SEQUENCE FROM N.A.
RP	TISSUE=PLACENTA;
RA	Iisogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA	Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA	Matsushima M., Hosori T., Raku Y., Kodaira H., Kondo H., Sugawara
RA	Takahashi M., Chiba Y., Ishida S., Murakami K., Ono Y., Takiguchi
RA	Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.
RA	Yamanoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.
RA	Niinomiya K., Iwayanagi T.;
RT	"NEDO human cDNA sequencing project.";
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBD databases.
RL	EMBL: AK027784; BAB55366.1; -
SO	SEQUENCE 358 AA; 41462 MW; 7822700C8E30CTE9 CRC64;

Query Match	39.38;	Score 699.5;	DB 4;	Length 358;
Best Local Similarity	42.68;	Pred. No. 9.6e-55;		
Matches 140;	Conservative 67;	Mismatches 113;	Indels 9;	Gaps 5;

QY	6	NLTPAG--NTEJLCRDKKITPOVEPLRYTTEFEGLTNGCLAMIPFOISKSFEITLK	64
Db	25	NRSDGPGKNTL---HNHFDIVLRYLLIIFVASILLNGLAAMIPEFHINKRSFITYLK	81
QY	65	NTVJSDLLMLTFPKPKILSDAKLTGRLPFRVCQVTSYVIFETMYTISLGLITDRQ	124
Db	82	NIYAADLLMTLTFEPRFVHDGFGPWFYKFLCYLCTRYSVLFPANNYTSIVFGGLISIDRYL	143
QY	125	KTRPFPKTSNKNLGGAKILSVVIMAFMFLSLDPLNMILTNROPDKVVKCSFPLSEGL	184
Db	142	KVMPFEGDSRAYNTTFTRKVLSCVWVIMAVLSELSRNIIITLNGQPTEDNIHDSKSLPLGV	201
QY	185	VMHLELVNVCQVIMFNFLVYVCYTLTLTKELRYSTYRTKGVCVPPRK--KVNNKVFIIIA	243
Db	202	KMHVAVTVNSCLFVAVALVILIGCIYIAISRHKRS--SRQTSOSSSKRRKHNDOSIRVVA	259
QY	244	VEFTCEVEFHARIPYTLQSOTRDVEFDCATENTLTLYVKESTLMLTSLNACLDPIIFYELCK	303
Db	260	VEFTCELPYHLCRIPIEFHSHDRLLDESAQKILTYCKEITLFLSACVWCDPIITYFPMCR	319
QY	304	SFRNSLT--SMLKCPNSATSLSDQNRKKE	330
Db	320	SFSRRLEKKSNIKRRESIRSLQSVRSE	348

RESULT	10	
Q9BY21		
ID	Q9BY21	PRELIMINARY; PRT; 358 AA.
AC	Q9BY21;	
DT	01-JUN-2001 (TrEMBLrel. 17, Created)	
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
DE	ORPHAN G PROTEIN-COUPLED RECEPTOR 87.	
GN	GPR87 OR GPR95.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	

```

RX MEDLINE=21172992; PubMed=11273702;
RA Wittenberger T., Schaller H.C., Hellebrand S.;
RT "An expressed sequence tag (est) data mining strategy succeeding in
RT the discovery of new g-protein coupled receptors."
RL J. Mol. Biol. 307:799-813(2001).
RN [12]
RP SEQUENCE FROM N.A.
RX MEDLINE=21458557; PubMed=11574159;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanli W.B., Arkhitko O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor
RT genes."
RL Gene 275:83-91(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF237763; AK01858.1; -.
DR EMBL: AF411114; AL26485.1; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECCEP_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECCEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 358 AA; 41435 MW; FDF157239B5D10F CRC64;

Query Match 39.1%; Score 694.5; DB 4; Length 358;
Best Local Similarity 42.2%; Pred. No. 2,7e-54;
Matches 139; Conservative 66; Mismatches 113; Indels 9; Gaps 5;

QY 6 NLTSPAG-NISLCTRDYKITQVLFPLLYTVLFVGLITNGLAMRIFFOIRSKSNFIIFLK 64
DB 25 NRSQSGPKNTTL--HNEFDIVLVPLVLLIFVASILNGLAWIFFHIRNKTSPFIYK 81
QY 65 NTVSDMLLTFPEPKILSDAKLGTPFTVCQTSVIFFTMYTISIFLGITIDRQ 124
DB 82 NIVADIMTLTFPRFRIYHAGFGWYFKTLCRTSVLFYANMTSIVFGLISIDRL 141
QY 125 KTRPFPTSNPKNLGAKILSVIWMFELSLPMLITNROPDRKNVKSFLSEFGL 184
DB 142 KYVPRFGDSRMYSITFTKVLSCVWYIMAVLSLPNIIITNGOPTEDNHDCKSLSPGLV 201
QY 185 VMHIVNYICQVIVINFLIVCYTLITKELYSYVTRGVKYPK-KVNVKVFIIIA 243
DB 202 KWHYAVTVYNSCLFVAVLIVLIGCYIAISRYIHS--SRQFISOSRRKHNOSIRVVA 259
QY 244 VFFICFVPHFARIPYLTQSQRDVFDCAEMTLFVKESTIMTSLNCLDPIYEFCK 303
DB 260 VFFICFVPHFARIPYLTQSQRDVFDCAEMTLFVKESTIMTSLNCLDPIYEFCK 319
QY 304 SFRNSLI--SMLKCPNSATSLSDNRKKE 330
DB 320 SFSRRLFKKSNIRTSIESIRLSQSVRSE 348

RESULT 11
Q99MT7 PRELIMINARY; PRT; 359 AA.
AC 099MT7;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR GPR87.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21172992; PubMed=11273702;
RA Wittenberger T., Schaller H.C., Hellebrand S.;
RT "An expressed sequence tag (est) data mining strategy succeeding in

```

```

RT the discovery of new g-protein coupled receptors."
RL J. Mol. Biol. 307:799-813(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF235366; AK01866.1; -.
DR MGD: MGI:1934133; Gpr87.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECCEP_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECCEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 359 AA; 41462 MW; 2EB313C273EFCDEA CRC64;

Query Match 38.6%; Score 685.5; DB 11; Length 359;
Best Local Similarity 41.7%; Pred. No. 1.7e-53;
Matches 136; Conservative 65; Mismatches 120; Indels 5; Gaps 3;

QY 8 TSAPGNTSICTRDYKITQVLFPLLYTVLFVGLITNGLAMRIFFOIRSKSNFIIFKNV 67
DB 26 SISEGSKNSTLHNKEDTILIPVLYIVFVASILNGLAWIFFHIRNKTSPFIYKNIY 85
QY 68 ISDMLITLTFPEPKILSDAKLGTPFTVCQTSVIFFTMYTISIFLGITIDRQKT 127
DB 86 VADLIMTLTFPRFRIYHAGFGWYFKTLCRTSVLFYANMTSIVFGLISIDRLKV 145
QY 128 RPFKTSNPKNLGAKILSVIWMFELSLPMLITNROPDRKNVKSFLSEFGLVWH 187
DB 146 KFGDSRMYSITFTKVLSCVWYIMAVLSLPNIIITNGOPTEDNHDCKSLSPGLAKWH 205
QY 188 EIVNYICQVIVINFLIVCYTLITKELYSYVTRGVKYPK-KVNVKVFIIIAVEF 246
DB 206 MAVTVYDSCLFVAVLIVLIGCYIAISRYIHS--SRQFISOSRRKHNOSIRVVAVF 263
QY 247 ICFVPHFARIPYLTQSQRDVFDCAEMTLFVKESTIMTSLNCLDPIYEFCKSR 306
DB 264 TCFPLPHICRIPFTFSNLDRLDESARKITLYCKEMTLFSLACNVCLDPIYEFCKSFS 323
QY 307 NSLI--SMLKCPNSATSLSDNRKKE 330
DB 324 RRLFKKSNIRTSIESIRLSQSVRSE 349

RESULT 12
Q9BE53 PRELIMINARY; PRT; 228 AA.
AC 09BE53;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN.
OS Macaca fascicularis (Crab eating macaque) (Cynomolpus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FRONTAL CORTEX;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB056816; BAB39342.1; -.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G_PROTEIN_RECCEP_FL_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECCEP_FL_2; 1.
SQ SEQUENCE 228 AA; 26356 MW; 47907F5DBEDD22C CRC64;

```


RA Yang W.S., Diehl J.R., Roubesh W.E.;
RT "Partial Sequence of Bovine Platelet-Activating Factor Receptor
RT Gene";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA He B., Tiemann U., Kanitz W., Weikard R., Laurent P., Schwerin M.,
RA Schmidt P.;
RT "Molecular characterization of bovine platelet-activating factor
RT receptor transcripts and their detection in different tissues of
RT cattle";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187321; AAF01439.2; .
DR EMBL; AJ295321; CAC43290.1; .
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
KW Receptor.
SQ SEQUENCE 342 AA; 39691 MW; 7C4236205AE937C9 CRC64;

Query Match 21.9%; Score 388.5; DB 6; Length 342;
Best Local Similarity 30.3%; Pred. No. 5.9e-27;
Matches 101; Conservative 63; Mismatches 136; Indels 31; Gaps 10;
QY 11 PGNSTLCRDYKQITOVLPFLYTVLFEGVLTNGLAMRIFQIRSKSNF--IIFLKNTV 67
DB 3 PNNFPRDSEERYT--LPIFYSTVFGVIANSVLWVFARLYPSKKNFKIKIFMVLNT 60
QY 68 ISDLMLITFPFKILSDAKLIGTGPLRTFCOVTSVIEFTWYISISFLGLITIDRYQKTT 127
DB 61 MADLLFLVTLPLFMIVYYNQGDWILPKFLCNLAGCFEFTNYCSVAFLAVITYNRFQAVT 120
QY 128 RPKFTSNPKNLGAKILSVTW-----AFWFLSLPMLITNRQPR--DKNVKCKSF 177
DB 121 RPIKTAQATTRKRGILSLIIVSVIGASVFEVLD-----STNREPNTKGSANITRC-F 174
QY 178 LKSEGLWMBEIVNYICOVIFMINFLIYVCYTLITKELYSYVTRGKGVPRKKVNVK 237
DB 175 EHYEKGSIPVLTIHIFLVFSFVLVLIILFCNLVITIRTLTQOVQIQRNAEYKRRAIMM- 233
QY 238 VEITIAVFFICFVPPHFAIRIPYTUSQTRDVPDCTAENTLFFVKESTLWLSLACLDPPI 297
DB 234 VCVTLAVFIIICFVPHHIVQLPWLAEI-GFQDTEFHQAINDAHQVTLCLSLSTNCVLDPII 292
QY 298 YFELCKSGFRNLSLML-----KCPNSATS 321
DB 293 YCFLLKKFRKHLTEKLYSMRESRC-SRATS 322

Search completed: September 6, 2002, 15:34:20
Job time: 238 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2002, 15:28:27 ; Search time 13.07 Seconds
(without alignments)
639.139 Million cell updates/sec

Title: US-09-827-937A-2

Perfect score: 1778

Sequence: 1 MOAVDNLTSPGNTSLCTRD.....SQDNRRKEDGGDPNEETPM 342

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfillset1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1778	100.0	342	3	US-08-852-824-2
2	823	46.3	333	4	US-09-221-456-2
3	823	46.3	333	4	US-09-558-740-2
4	797	43.4	333	2	US-08-812-871-1
5	772	43.4	325	2	US-08-467-948A-29
6	772	43.4	325	3	US-08-467-947A-29
7	772	43.4	338	3	US-08-988-876-8
8	772	43.4	338	4	US-09-303-524A-2
9	679.5	38.2	358	3	US-08-988-876-3
10	546.5	30.7	293	2	US-08-467-948A-6
11	546.5	30.7	293	3	US-08-467-947A-6
12	488	27.4	319	1	US-08-702-344-28
13	410.5	23.1	326	1	US-08-118-270-39
14	410.5	23.1	326	5	PCT-US93-08528-39
15	392.5	22.1	342	5	US-08-988-876-9
16	379.5	21.3	361	1	US-08-383-750-4
17	379.5	21.3	361	1	US-08-352-678-4
18	379.5	21.3	361	5	PCT-US93-08636-4
19	376	21.1	348	5	US-08-852-824-17
20	374.5	21.1	381	1	US-08-467-125-2
21	374.5	21.1	381	2	US-08-911-320A-2
22	374.5	21.1	381	4	US-09-217-101-2
23	349.5	19.7	302	3	US-08-467-948A-30
24	349.5	19.7	302	3	US-08-467-947A-30
25	339	19.1	344	2	US-08-467-948A-8
26	339	19.1	344	3	US-08-467-947A-8
27	337	19.0	68	4	US-08-905-223-327

28	329.5	18.5	339	1	US-08-153-848-44	Sequence 44, Appl
29	329.5	18.5	339	2	US-08-812-871-3	Sequence 3, Appl
30	329.5	18.5	339	2	US-09-299-843A-44	Sequence 44, Appl
31	329.5	18.5	339	4	US-09-088-337B-44	Sequence 44, Appl
32	329.5	18.5	339	5	PCT-US93-11153-44	Sequence 44, Appl
33	329.5	18.5	339	5	PCT-US95-07180-2	Sequence 6, Appl
34	329	18.5	359	1	US-08-041-219A-6	Sequence 6, Appl
35	329	18.5	359	1	US-08-417-122-6	Sequence 6, Appl
36	327.5	18.4	395	1	US-08-476-000-2	Sequence 2, Appl
37	327.5	18.4	395	1	US-08-472-840-2	Sequence 2, Appl
38	327.5	18.4	395	1	US-08-476-976-2	Sequence 2, Appl
39	327.5	18.4	395	2	US-08-474-410-2	Sequence 2, Appl
40	325.5	18.3	395	3	US-08-486-673B-2	Sequence 2, Appl
41	325.5	18.3	395	4	US-08-486-673B-5	Sequence 5, Appl
42	325.5	18.3	399	1	US-08-476-000-61	Sequence 61, Appl
43	325.5	18.3	399	1	US-08-472-840-61	Sequence 61, Appl
44	325.5	18.3	399	2	US-08-476-976-61	Sequence 61, Appl
45	325.5	18.3	399	2	US-08-476-976-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1	US-08-852-824-2	Application US/08852824C
Sequence 2, Applicant: Li et al.	Patent No. 6060272	GENERAL INFORMATION:
FILE REFERENCE: 1488.1220000	CURRENT APPLICATION NUMBER: US/08/852,824C	
CURRENT FILING DATE: 1997-05-04	NUMBER OF SEQ ID NOS: 18	
SOFTWARE: PatentIn Ver. 2.0	SEQ ID NO 2	
LENGTH: 342	TYPE: PRT	
ORGANISM: genomic	US-08-852-824-2	
Query Match	100.0%: Score 1778; DB 3; Length 342;	
Best Local Similarity	No. 1.3e-144;	
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY 1	MOAVDNLTSPGNTSLCTRDYKITQVLPFLYTVLFFVGLITNGLAMRIFFQIRSNFT 60	
DB 1	MOAVDNLTSPGNTSLCTRDYKITQVLPFLYTVLFFVGLITNGLAMRIFFQIRSNFT 60	
OY 61	IFLKNTVSDLMILTFEPKILSDAKLGTGCPRTFVCQVTSVFYFTMYTISIFLGIT 120	
DB 61	IFLKNTVSDLMILTFEPKILSDAKLGTGCPRTFVCQVTSVFYFTMYTISIFLGIT 120	
OY 121	DRYQTRTFKTSNPNLGAKITLSVIAFMFLSLPMNMLTNRPDRKNVKKCSFLKS 180	
DB 121	DRYQTRTFKTSNPNLGAKITLSVIAFMFLSLPMNMLTNRPDRKNVKKCSFLKS 180	
OY 181	EEGLVWEIIVNYICQVIFMIFNLIVCYTLTKELYSRVTRGVGVKRVKVVVF 240	
DB 181	EEGLVWEIIVNYICQVIFMIFNLIVCYTLTKELYSRVTRGVGVKRVKVVVF 240	
OY 241	IIAVFFICVPHFARIPYTLSTQTRVPCDTAENTLFYKKESTLMTLSLNACDPFIYF 300	
DB 241	IIAVFFICVPHFARIPYTLSTQTRVPCDTAENTLFYKKESTLMTLSLNACDPFIYF 300	
OY 301	LCKSFRNLSLMKCPNSATSLSDNRRKEDGGDPNEETPM 342	
DB 301	LCKSFRNLSLMKCPNSATSLSDNRRKEDGGDPNEETPM 342	
RESULT 2	US-09-221-456-2	

ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: filed Herewith
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0237 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: MML3D701
CLONE: 568987
US-08-812-871-1

Query Match 44.8%; Score 797; DB 2; Length 333;
Best Local Similarity 47.8%; Pred. No. 7,7e-61;
Matches 151; Conservative 57; Mismatches 106; Indels 2; Gaps 1;

OY 17 CTSDYKITOVLPFLYVLFVGLITNGLAMRIFPOIRSKSNFIPLKNTIVISDLMLT 76
DB 15 CPDRTRIVQVLPFLYVLFVGLITNGLAMRIFPOIRSKSNFIPLKNTIVISDLMLT 74
OY 77 FPKKILSDALGGLPRTFVCQVTSVFYFTMYISISFLGLITDRQKTRPKTSMPK 136
DB 75 LPRKILSDSHLAWQMLAFVCRSSSVIFETMYGIVLGLIADRFKILIRPLNIFLK 134
OY 137 NLGAKILSVIVAFMFLSLPNMILTNROPDRKNVKKCSFLKSEFGLVWHEIYVICOV 196
DB 135 KPFKATVSLFIFLFLFSLPILMILSKNKEPSSVKKCAKGLPLGLKMHQNNNICOF 194
OY 197 IFWNLIVIVCYTLITKELYSYVTRGVGKVRKKNVVFIIIAVFICFVPHFRAR 256
DB 195 IFWTLVILMLVFYVLAKKYDYSYRKSCKDKRKNKKLECKVVFVVFVFCFAPHFRAR 254
OY 257 IPTVLSOTRVPFCTAENTLFYVKESTLMLTSLNACDPLFYFFLCKSFRLSLMLKCP 316
DB 255 VPTSHQTNKTKCRLQNOFLIAKETTLFLAATNICMDPLISFLCKKFTKELPCMO--G 312
OY 317 NSATSLSDNRKKEOD 332
DB 313 RKTASSQENHSSQTD 328

RESULT 5
US-08-467-948A-29
Sequence 29, Application US/08467948A
Patent No. 5998164
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG

APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BUTT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-948A-29

Query Match 43.4%; Score 772; DB 2; Length 325;
Best Local Similarity 47.5%; Pred. No. 1e-58;
Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

OY 6 NLTSAPGNTSLCTRDYKITOVLPFLYVLFVGLITNGLAMRIFPOIRSKSNFIPLK 65
DB 2 NSTSTQPPDESCSNLITQOIIIPVLYCMVFTAGIILNVGSGWIFRYVSSKSFIIYLN 61
OY 66 TVISDLMLITPEPKILSDAKLGTGRLTFVCOVTSVFYFTMYISISFLGLITDRYOK 125
DB 62 IVIADPVMSLTFPEPKILSDGSLGPMQANFVCRVSAVLVFNMYVSVIFGLISFDRYK 121
OY 126 TTRPKTSMPKNDLGAIIISVIVAFMFLSLPNMILTNROPDRKNVKKCSFLKSEGLV 185
DB 122 IVKPLMTSFIQSSYSKLSIVYIMLMLLAVNIIITNOSVREVIQKIEKSELGRK 181
OY 186 WHEIYVICOVIFWNLIVIVCYTLITKELYSYVTRGVGKVRKKNVVFIIIAVF 245
DB 182 WHKASNYIFVAIFWIFELIIVFTYITIKIFSHLKSNSVKKSSRNIFSVFVF 241
OY 246 FICFVPHFRARIPYTLSDTRVFDCTAENTLFYVKESTLMLTSLNACDPLFYFFLCKSF 305
DB 242 FVCFVPHFRARIPYTKSQAHEAHSCSKELRYMKKEFTLLSANVNCIDPLIYFFLCQPF 301
OY 306 RNSLISMLKCPNSA 319
DB 302 REILCKKIHPIKA 315

OY 186 WHEIINVOQVWFMEFLIVICVTITTELYSRYTRGVAPRRKVVKEIIIAVF 245
DB 183 MHKASNIFYVAIFWFIYFLLILVIPTYAITIKKIFSHLKSSNNSTSVKKSSRNFTSFVVF 242

OY 246 FICEVPFHARIPYTLSOTRDVEDCTAENTLFPVKESTLMLTSLNACLDPEFYFFELCKSP 305
DB 243 FVCDFPVHJARIPYTKRSOFEAHNSCOSKELRMYMKEPTILLSANANCCLDPIITYFFLCQPF 302

OY 306 RNSLISMCLKCPNSA 319
DB 303 REICKKLHIPLKA 316

RESULT 8
US-09-303-524A-2
Sequence 2, Application US/09303524A
Patent No. 6238873
GENERAL INFORMATION:
APPLICANT: CHAMBERS, JONATHAN K.
APPLICANT: STEWART, BRIAN R.
APPLICANT: AMES, ROBERT S.
APPLICANT: SARAU, HENRY M.
APPLICANT: POLEY, JIM
APPLICANT: ARNOLD, ANNE ROMANIC
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN THE HUMAN KIAA0001
TITLE OF INVENTION: RECEPTOR AND LIGANDS THEREOF
FILE REFERENCE: GP50007
CURRENT APPLICATION NUMBER: US/09/303,524A
CURRENT FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: 60/083,957
PRIOR FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 338
TYPE: PRT
ORGANISM: Homo sapiens
US-09-303-524A-2

[illegible]

```

US-08-988-876-3
: Sequence 3, Application US/08988876
: Patent No. 6063596
:
: GENERAL INFORMATION:
: APPLICANT: Lal, Preeti
: APPLICANT: Bandman, Olga
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Yue, Henry
: TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
: TITLE OF INVENTION: WITH IMMUNE RESPONSE
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/988,876
: FILING DATE: Herewith
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PP-0441 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-855-0555
: TELEFAX: 650-845-4166
: TELEX:
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 358 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: PROSTUT09
: CLONE: 1650519
:
US-08-988-876-3

```

[illegible]

OY 197 IFMIFNFIIVCYLTLE-----LYRSRFRGRGVKPRKKVNVKVIILIAVEFCVP- 251
Dd 195 IFMFVFELMLVFVVYVANKRWILLIESPVRERKTKTSMKAKAYLLSWLSLCLVLHFFSPE 256

OY 252 FHFARIPFTLSQTRDVDCETENLFLFYKESTLW 265
Db 255 FHILTVMKPTIRLT--VDCKT-NCLLKLRKOLSEFW 284

RESULT 12
US-08-702-344-28

```

1      Sequence 28, Application US/08702344
2      Patent No. 5723315
3
4      GENERAL INFORMATION:
5      APPLICANT: Jacobs, Kenneth
6      APPLICANT: McCoy, John
7      APPLICANT: LaVallie, Edward
8      APPLICANT: Racie, Lisa
9      APPLICANT: Merberg, David
10     APPLICANT: Treacy, Maurice
11     APPLICANT: Spaulding, Vikki
12     TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
13     TITLE OF INVENTION: ENCODING THEM
14     NUMBER OF SEQUENCES: 37
15     CORRESPONDENCE ADDRESS:
16     ADDRESSEE: Genetics Institute, Inc.
17     STREET: 87 CambridgePark Drive
18     CITY: Cambridge
19     STATE: Massachusetts
20     COUNTRY: U.S.A.
21     ZIP: 02140
22
23     COMPUTER READABLE FORM:
24     MEDIUM TYPE: floppy disk
25     COMPUTER: IBM PC compatible
26     OPERATING SYSTEM: PC-DOS/MS-DOS
27     SOFTWARE: PatentIn Release #1.0, Version #1.30
28     CURRENT APPLICATION DATA:
29     APPLICATION NUMBER: US/08/702,344
30     FILING DATE:
31     CLASSIFICATION: 536
32
33     ATTORNEY/AGENT INFORMATION:
34     NAME: Brown, Scott A.
35     REGISTRATION NUMBER: 32,724
36     TELECOMMUNICATION INFORMATION:
37     TELEPHONE: (617) 498-8224
38     TELEFAX: (617) 876-5851
39
40     INFORMATION FOR SEQ ID NO: 28:
41     SEQUENCE CHARACTERISTICS:
42     LENGTH: 319 amino acids
43     TYPE: amino acid
44     STRANDEDNESS:
45     TOPOLOGY: linear
46
47     MOLECULE TYPE: protein
48
49     US-08-702-344-28

```

Query Match	27.48;	Score 488;	DB 1;	Length 319;
-------------	--------	------------	-------	-------------

Best Local Similarity 34.5%; Pred. No. 1.8e-34;
Matches 112; Conservative 62; Mismatches 125; Indels 26; Gaps 9;

OY 13 NTSLCTBDYKITYQLVLEFLTYLVLFVFGVLITNGLMARIFPQIRKSANFI -IFLKATVTISDL 71
 : : : : : : : : : : : : : : : : : :
Dd 3 NSSEFCBPVKDLEF-FYFFYFLVFVGLTIGSCFATMAFIQNTHHRCVSIIYLILLTADF 61
 : : : : : : : : : : : : : : : : : :
OY 72 LMLIFPPKKILSDAKLGGF--LRTPCQVTSVAFETYMTSISFLGILTIDRQKTTR 129
 : : : : : : : : : : : : : : : : : :
Dd 62 LTTALPAKIYVD--LGVAAPKLKIFHQVTAACIYNMYSIIFLFVSDICRLDTUHS 119
 : : : : : : : : : : : : : : : : : :
OY 130 FKTSNPVKLLDAKILSYIVAMFMLSPPNLIINRDPRDKNVAKCSFLSEGVVHEI 189
 : : : : : : : : : : : : : : : : : :
Dd 120 KTIPIQDEPGAKMISTVMYLAIVLLINPMNIPIKDIKEKSNVGCSEFKFEERRNNHL 179

```

QY 190 VNYCQYIEMFNE-LIIVYCTLTLEKELYSYATRGVAPR-KKVVAVFIIIAVEFI 247
    |:|| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 180 TNEICVAIF-LNESAITLISNCVITROLRYR---KQENMYPNVKKALINILLVTTCYII 234
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 248 CEFVFEHARIPYTSQTRDVEDCTCAENUTLEPVKESTLTLTLNACDLPFTYFCLKSFRN 307
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 235 CEFVRYHIVRIDPYTSLQTEVITDCSTRISLRAKEATILLAVSNLCFDPILYHLRAFRS 294
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 308 SLI-----SMLCPNSA 319
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 295 KYTETFPASPKETKQKEKLEKRENNNA 319
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 13
US-08-118-270-39
; Sequence 39, Application US/08118270

Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
ATTORNEY/AGENT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF INVENTION: 348
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-39

Query Match	23.18;	Score 410.5;	DB 1;	Length 326;
-------------	--------	--------------	-------	-------------

Best Local Similarity 32.2%; Pred. No. 7.7e-28;
Matches 106; Conservative 65; Mismatches 137; Indels 21; Gaps 9;

[illegible]

Db 121 SLVIWAIVAASAYFLVMDSTNVSNKAGSGNITRC--FEYKESKPVLIH-----IC 174
QY 195 QVI-FWNLFLVICYTLTLELRSYVRGKVPKRVNKKVFLIIAIFCIVP 253
Db 175 IVLGEFFVLLILCNLIIHTLLRGPKQORNAEV--RRALMVCYIAVFIICVPH 233
QY 254 FARIPYTLISQTRDVEDCTAENTLFYVKESTLWLTSLNACLDPEFIYFLCKSFNLSIML 313
Db 234 MVQLPMTLAEI-GMPPSSNHQAINDAHQVTLCLLSTNCVLDPVICYFLTKFRKHLSEKL 292
QY 314 KCPNSATSLSDNKKKEDGSDPNEETPM 342
Db 293 NIMRSSQKCSRVTRDTGTETMAIPINHTPV 321

RESULT 14
PCT-US93-08528-39
Sequence 39, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-39

Query Match 23.1%; Score 410.5; DB 5; Length 326;
Best Local Similarity 32.2%; Pred. No. 7.7e-28;
Matches 106; Conservative 65; Mismatches 137; Indels 21; Gaps 9;

QY 27 LFPLLYVLFVGLITNGIAMIIFFOI--RSKSNFI-IFLKNTVISDLMILTFPKIISD 84
Db 1 LEPVIVSIIFVGLIANGYVLMVFARLVPKSKNEIKIFMVLNLTVDLFLITLPLMIYY 60
QY 85 AKUGTGLRPFVCOVTSIFFTMTISISFLGTTIDRYQKTRPFKTSNPKNLGAKIL 144
Db 61 SNGGNMFLPKFLMACLFPINTYCSVAFLGVITYNRFOAVKYPDKTAQATRRKGIAL 120
QY 145 SVYVW-----AFMELLSLPMILTNROPDRKNVKKCSFLSESG---LVWHELVANIC 184

Db 121 SLVIWAIVAASAYFLVMDSTNVSNKAGSGNITRC--FEYKESKPVLIH-----IC 174
QY 195 QVI-FWNLFLVICYTLTLELRSYVRGKVPKRVNKKVFLIIAIFCIVP 253
Db 175 IVLGEFFVLLILCNLIIHTLLRGPKQORNAEV--RRALMVCYIAVFIICVPH 233
QY 254 FARIPYTLISQTRDVEDCTAENTLFYVKESTLWLTSLNACLDPEFIYFLCKSFNLSIML 313
Db 234 MVQLPMTLAEI-GMPPSSNHQAINDAHQVTLCLLSTNCVLDPVICYFLTKFRKHLSEKL 292
QY 314 KCPNSATSLSDNKKKEDGSDPNEETPM 342
Db 293 NIMRSSQKCSRVTRDTGTETMAIPINHTPV 321

RESULT 15
US-08-988-876-9
Sequence 9, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 49443
US-08-988-876-9

Query Match 22.1%; Score 392.5; DB 3; Length 342;
Best Local Similarity 30.7%; Pred. No. 2.8e-26;
Matches 103; Conservative 66; Mismatches 146; Indels 21; Gaps 9;

QY 20 DYKITOVLPFLLYVLFVGLITNGIAMIIFFOI--RSKSNFI-IFLKNTVISDLMILTN 76
Db 10 DSEFRTLEFPYISIFVGLIANGYVLMVFARLVPKSKNEIKIFMVLNLTVDLFLIT 69

This Page Blank (uspio)